

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 19:46:15 ; Search time 7.72/27 Seconds

(without alignments)

205.411 Million cell updates/sec

Title: US-09-546-136-1.

Perfect score: 52

Sequence: 1 MKQAFVFED 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Genesed_19Jun03 :*

1: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1980 DAT:*

2: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1981 DAT:*

3: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1982 DAT:*

4: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1983 DAT:*

5: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1984 DAT:*

6: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1985 DAT:*

7: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1986 DAT:*

8: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1987 DAT:*

9: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1988 DAT:*

10: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1989 DAT:*

11: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1990 DAT:*

12: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1991 DAT:*

13: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1992 DAT:*

14: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1993 DAT:*

15: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1994 DAT:*

16: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1995 DAT:*

17: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1996 DAT:*

18: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1997 DAT:*

19: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1998 DAT:*

20: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA1999 DAT:*

21: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA2000 DAT:*

22: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA2001 DAT:*

23: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA2002 DAT:*

24: /SIDS1/geodata/genedata/geneseq/geneseqp-emb1/AA2003 DAT:*

RESULT 1

AAW37236

ID AAW37236 standard; peptide: 10 AA.

XX

AC AAW37236;

XX

DT 17-JUN-1998 (first entry)

XX

DE Partial sequence of botulinum neurotoxin serotype E associated protein.

XX

KW Clostridia; botulinum toxin; neurotoxin; serotype E; vaccine;

KW antibody; acetylcholine; presynaptic nerve.

XX

OS Clostridium botulinum.

XX

PN W09801754 -A1.

XX

PD 15-JAN-1998

PF 08-JUL-1996; 96WO-US11383.

XX

PR 08-JUL-1996; 96WO-US11383.

XX

PA (UWMA) UNIV MASSACHUSETTS DARTMOUTH.

XX

PI Singh BR, Zhang Z;

XX

DR WPI: 1998-101196/09.

PT Polypeptide complex synthesised by Clostridia - useful in, e.g.

PT producing vaccines for protecting animals against serotype E

PT neurotoxin mutant human IKBKA

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	19 AAW37236	Partial sequence of Thermus filiformis
2	34	65.4	374	22 AAB30355	Human protein sequ
3	34	65.4	406	22 AAB94069	Human IKAP protein sequ
4	34	65.4	537	22 AAB95734	Human IKAP protein
5	34	65.4	1332	20 AAY01084	Human protein sequ
6	34	65.4	1332	22 AAB9310	Human IKAP, Homo
7	34	65.4	1332	22 AAB66345	Wild-type human IK
8	34	65.4	1332	23 ABB89452	Mutant human IKBKA
9	34	65.4	1332	23 ABB98453	

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	19 AAW37236	Partial sequence of Thermus filiformis
2	34	65.4	374	22 AAB30355	Human protein sequ
3	34	65.4	406	22 AAB94069	Human IKAP protein sequ
4	34	65.4	537	22 AAB95734	Human IKAP protein
5	34	65.4	1332	20 AAY01084	Human protein sequ
6	34	65.4	1332	22 AAB9310	Human protein sequ
7	34	65.4	1332	22 AAB66345	Human IKAP, Homo
8	34	65.4	1332	23 ABB89452	Wild-type human IK
9	34	65.4	1332	23 ABB98453	Mutant human IKBKA

Claim 17; Page 3; 38pp; English.

A new peptide complex synthesised by Clostridia bacteria comprises the serotype E botulinum neurotoxin and five neurotoxin associated peptides of molecular weights 118, 80, 65, 40 and 18 kDa respectively. The present sequence represents a partial sequence of the 18 kDa peptide. Also claimed are: (1) detecting the serotype E neurotoxin complex in biological samples by: (a) contacting with an antibody or polypeptide specifically binding to a polypeptide of the complex, and (b) detecting antibody- or polypeptide-bound polypeptide, indicating the presence of serotype E neurotoxin; (2) an antibody binding to the complex, or one of the five neurotoxin associated polypeptides, and (3) polypeptides isolated from the complex. The complex can be used to produce therapeutic agents for treating diseases resulting from excessive acetylcholine release from presynaptic nerve terminals causing undesirable contraction of smooth or skeletal muscle cells and resulting in, e.g. spasmodic torticollis, essential tremor, spasmodic dysphonia, charley horse, strabismus, blepharospasm, oromandibular dystonia, spasms of the sphincters of the cardiovascular, gastrointestinal or urinary systems, tardive dyskinesia, profuse sweating, lacrimation or mucous secretion. The complex can also be used to produce therapeutics for treating spasticity occurring secondary to brain ischaemia, traumatic injury of the brain or spinal cord, tension headaches, pain caused by sporting injuries or arthritic contractions. The complex may further be used, within a carrier to prepare vaccines, useful for, e.g. vaccinating animals against serotype E neurotoxin. The polypeptides can be used for testing foodstuff, or diagnosing vertebrate gastrointestinal, blood or tissue samples, for infection with serotype E neurotoxin, useful in preventing botulism.

Sequence	10 AA:	Score	52;	DB 19;	Length 10;	
SSQ	Query Match	100.0%				
	Best Local Similarity	100.0%	Pred. No.	0.00037;		
	Matches 10;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MKQAFVFEED	10			
Ddb	1	MKQAFVFEED	10			

RESULT 2

AC AAB30325;
 XX
 DDT 12-FEB-2001 (first entry)
 XX
 DE *Thermus filiformis* Tfii methylase.
 XX
 KW Tfii: methylase; restriction endonuclease; nucleic acid cleavage.

U.S. Patent and Trademark Office
Reg. No. 4,330,088
A
THERMUS FILIFORMIS.

17-OCT-2000.

07-1999; 99US-030681.
XX XX PA (NEW) NEW ENGLAND BIOLABS INC.
XX XX PA

Homo sapiens
OS XXX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XXX
PPF 28-JUL-2000; 20000SP-0116126.

PR 29-JUL-1999; 990IP-0248036.
 PR 27-AUG-1999; 990IP-0300253.
 PR 11-JAN-2000; 2000IP-0118776.
 PR 02-MAY-2000; 2000IP-0183767.
 PR 09-JUN-2000; 2000IP-0241899

(HELI-) HELIX RES INST.
PA
XX
Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PPI
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PPI
XXX
DDR
WPI; 2001-318749/34.
XXX

PPT full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the

XX Claim 8; SEQ ID 14254; 2537pp + CD ROM; English.
XXX
XXX The present invention describes primer sets for synthesising 5602
XXX full-length cDNAs defined in the specification. Where a primer set
XXX comprises: (a) an oligo-dT primer and an Oligonucleotide complementary
XXX to the complementary strand of a Polynucleotide which comprises one of
XXX the 5602 nucleotide sequences defined in the specification, where the
XXX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XXX

complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination the 5'-end sequence/3'-end sequence is selected from those defined in the specification.

CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 CC represent oligonucleotides, all of which are used in the exemplification CC of the present invention.

XX Sequence 406 AA;

Query	Match	Score	DB	Length
	Best Local Similarity	65.4%	22;	406;
	Matches	60.0%	Pred. No.	95;
		2;	Mismatches	2;
			Indels	0;
			Gaps	0;

Qy 1 MKQAFVFEFD 10

Db 314 LKVLFLEFFD 323

RESULT 4
AAB95734

ID AAB95734 standard; Protein: 537 AA.

XX XX AC

XX DT

XX Human protein sequence SEQ ID NO:18619.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI: 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX PS Claim 8: SEQ ID 18619; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the 5'-end sequence comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy, CC in gene therapy, the primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded, CC the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 CC represent oligonucleotides, all of which are used in the exemplification CC of the present invention.

XX Sequence 537 AA;

SO Query Match

Score 34; DB 22; Length 537;

Best Local Similarity 60.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 2; Mismatches 2;

Indels 0; Gaps 0;

Qy 1 MKQAFVFEFD 10

Db 445 LKVLFLEFFD 454

RESULT 5

AAY01084

ID AAY01084 standard; Protein: 1332 AA.

XX XX AC

XX AAY01084;

DT

09-JUN-1999 (first entry)

XX DE

XX Human IKAP protein sequence.

KW IKAP; human; cellular signal transduction regulator;

KW transcriptional activation regulator; translatable transcript.

XX OS

XX Homo sapiens.

XX PN

US5891719-A.

XX PD

06-APR-1999.

XX XX

PF

16-NOV-1997; 97US-0971244.

XX PR

16-NOV-1997; 97US-0971244.

XX PA

(TULRA-) TULARIK INC.

XX XX

PI

Baeuerle P, Cohen L;

XX DR

WPI: 1999-253865/21.

DR

N-PSDB; AAX28035.

XX XX

PT

Isolated, recombinant cDNA sequences encoding human IKAP

PT

polypeptides - useful for regulating cellular signal transduction

XX

PS

Claim 12; Column 9-18; 15pp; English.

XX

CC

Query Match 65.4%; Score 34; DB 20; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFVFEFD 10
 Db 1240 LKVLFLEFEF 1249

RESULT 6
 AAB93160
 ID AAB93160 standard; Protein: 1332 AA.
 XX
 AC AAB93160;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEO ID NO:12083.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-030253.
 PR 11-JAN-2000; 2000JP-0112776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI: 2001-158378/16.
 XX
 PT Novel human kinase IKAP polypeptide useful in diagnosis, therapy,
 PR biopharmaceutical industry and for screening for modulators of the
 PR polypeptide.
 PT Cohen L, Bauerle P;
 XX
 PS Claim 24; Column 17-24; 15pp; English.
 XX
 CC The present invention provides the human IKAP protein. This is involved
 CC in signal transduction pathways, where it binds to NIK and results in the
 CC activation of transcription factors. The protein and its coding sequence
 CC can be used in disease diagnosis and therapy, as well as in the
 CC biopharmaceutical industry.
 XX
 SQ Sequence 1332 AA;

Query Match 65.4%; Score 34; DB 22; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFVFEFD 10
 Db 1240 LKVLFLEFEF 1249

RESULT 7
 AAB66345
 ID AAB66345 standard; Protein: 1332 AA.
 XX
 AC AAB66345;
 XX
 DT 05-APR-2001 (first entry)
 XX
 DE Human IKAP.
 XX
 KW Human; IKAP; signal transduction; NIK binding activity;
 KW transcription factor; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6172195-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 06-APR-1999; 99US-0286891.
 XX
 PR 16-NOV-1997; 97US-0971244.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Cohen L, Bauerle P;
 XX
 DR WPI: 2001-158378/16.
 DR N-PSDB: AAF29756.

CC Novel human kinase IKAP polypeptide useful in diagnosis, therapy,
 PR biopharmaceutical industry and for screening for modulators of the
 PR polypeptide.
 XX
 PS Claim 24; Column 17-24; 15pp; English.
 XX
 CC The present invention provides the human IKAP protein. This is involved
 CC in signal transduction pathways, where it binds to NIK and results in the
 CC activation of transcription factors. The protein and its coding sequence
 CC can be used in disease diagnosis and therapy, as well as in the
 CC biopharmaceutical industry.
 XX
 SQ Sequence 1332 AA;

Query Match 65.4%; Score 34; DB 22; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFVFEFD 10
 Db 1240 LKVLFLEFEF 1249

RESULT 8
 ABB98492
 ID ABB98492 standard; Protein: 1332 AA.
 XX
 AC ABB98492;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Wild-type human IKBKAP.
 XX
 SQ Sequence 1332 AA;

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX

KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.
 XX
 OS Homo sapiens.
 XX
 PN WO200259381-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 07-JAN-2002; 2002WO-US00473.
 XX
 PR 06-JAN-2001; 2001US-260080P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Slaugenhoupt, S., Gusella, JF;
 XX
 WPI: 2002-674806/72.
 DR N-PSDB; ABQ80570.
 XX
 PT New IKBKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes
 PT or prenatal diagnosis.
 XX
 PS Claim 8; Fig 8; 109pp; English.
 XX
 CC The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
 CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
 CC are associated with FD. The mutation associated with the major haplotype
 CC of FD, FDI mutation, is a base pair (bp) mutation, where the thymine
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
 CC patients, although they continue to express varying levels of wild-type
 CC message in a tissue-specific manner. The mutation associated with the
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
 CC nucleotide at bp 2337 (bp 73 of exon 19) is replaced with a cytosine.
 CC This bp mutation causes an arginine to proline missense mutation (R696P)
 CC in the IKBKAP protein, which is predicted to disrupt a potential
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
 CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
 CC gene maps to chromosome 9q31. The present sequence is the wild-type human
 CC IKBKAP protein sequence.
 XX
 SQ Sequence 1332 AA;

Query Match 65.4%; Score 34; DB 23; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKQAFYEFID 10
 :1:|||||
 Db 1240 LKVLFLEFID 1249

RESULT 9
 ABB98493 ID AAO15505 standard; protein: 1332 AA.
 XX
 AC ABB98493;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Mutant human IKBKAP.
 KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-day syndrome; mutant;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
 KW mutein.
 XX
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT Misc-difference 696
 FT /note= "Wild-type Arg replaced by Pro"
 XX
 PN WO200259381-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 07-JAN-2002; 2002WO-US00473.
 XX
 PR 06-JAN-2001; 2001US-260080P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Slaugenhoupt, S., Gusella, JF;
 XX
 WPI: 2002-674806/72.
 DR N-PSDB; ABQ80570.
 XX
 PT New IKBKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes
 PT or prenatal diagnosis.
 XX
 PS Claim 9; Page 7; 109pp; English.
 XX
 CC The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
 CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
 CC are associated with FD. The mutation associated with the major haplotype
 CC of FD, FDI mutation, is a base pair (bp) mutation, where the thymine
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
 CC patients, although they continue to express varying levels of wild-type
 CC message in a tissue-specific manner. The mutation associated with the
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
 CC nucleotide at bp 2337 (bp 73 of exon 19) is replaced with a cytosine.
 CC This bp mutation causes an arginine to proline missense mutation (R696P)
 CC in the IKBKAP protein, which is predicted to disrupt a potential
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
 CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
 CC gene maps to chromosome 9q31. The present sequence is the mutant human
 CC IKBKAP protein sequence.
 CC Note: the present sequence was not shown in the specification, but was
 CC derived from the human wild-type IKBKAP sequence given in Fig 8.
 XX
 SQ Sequence 1332 AA;

Query Match 65.4%; Score 34; DB 23; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKQAFYEFID 10
 :1:|||||
 Db 1240 LKVLFLEFID 1249

RESULT 10
 AAO15505 ID AAO15505 standard; protein: 1332 AA.
 XX
 AC AAO15505;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Human I-kappa beta associated protein (IKAP).
 XX
 KW Human; single nucleotide polymorphism; SNP;
 KW bronchial asthma;
 KW I-kappa beta associated protein; IKAP; infant bronchial asthma.
 XX
 OS Homo sapiens.

PN WO200259305-A1.
 XX 01-AUG-2002.
 XX 25-JAN-2002; 2002WO-JP00540.
 XX 25-JAN-2001; 2001JP-0017076.
 PR (SAKA) ORSUKA PHARM CO LTD.
 XX PI Nakamura Y, Tamari M;
 XX WPI; 2002-557950/59.
 DR N-PSDB; ARI44190.
 XX PT Detection of specific single nucleotide polymorphisms in human I-kappa beta associated protein for analysis of etiology of bronchial asthma
 XX PS Claim 3: Page 39-45; 60pp; Japanese.
 XX CC The invention comprises a method for detecting single nucleotide polymorphisms (SNPs) in genes associated with human bronchial asthma. The method specifically refers to detecting polymorphisms in the gene encoding human I-kappa beta associated protein (IKAP). The invention also comprises primers and probes for use in the method of the invention. The method of the invention is useful for analysis of the etiology of bronchial asthma (especially infant bronchial asthma). The present amino acid sequence represents the human I-kappa beta associated protein.
 SQ Sequence 1332 AA;
 Query Match 65.4%; Score 34; DB 23; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX OS Neisseria gonorrhoeae amino acid sequence SEQ ID 4492.
 XX KW Antibacterial; infection; vaccine; gene therapy.
 XX OS Neisseria gonorrhoeae.
 PN WO200279243-A2.
 XX PD 10-OCT-2002.
 XX PF 12-FEB-2002; 2002WO-IB02069.
 XX PR 12-FEB-2001; 2001GB-0003424.
 PA (CHIR-) CHIRON SPA.
 XX PI Fontana MR, Pizza M, Masignani V, Monaci E;
 XX WPI; 2003-058415/05.
 DR N-PSDB; ABZ3951.
 XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection -
 XX PS Disclosure; Page 517; 815pp; English.

XX CC The present invention relates to proteins from *Neisseria gonorrhoeae*.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention.
 XX SQ Sequence 99 AA;
 Query Match 63.5%; Score 33; DB 24; Length 99;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
 ID ABB61497 standard; Protein: 534 AA.
 XX AC ABB61497;
 QY 1 MKQAFVFEFD 10
 :||| |||||
 Db 40 VQRATGFEFD 49

RESULT 12
 ID ABB61497 standard; Protein: 534 AA.
 XX AC ABB61497;
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 11283.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX PI DR WPI; 2001-656680/75.
 DR N-PSDB; ABL05600.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -
 PT XX Disclosure; SEQ ID NO 11283; 21pp + Sequence Listing; English.
 XX PS 01-MAR-2003 (first entry)
 DE N. gonorrhoeae amino acid sequence SEQ ID 4492.
 XX KW Antibacterial; infection; vaccine; gene therapy.
 XX OS Neisseria gonorrhoeae.
 PN WO200279243-A2.
 XX PD 10-OCT-2002.
 XX PF 12-FEB-2002; 2002WO-IB02069.
 XX PR 12-FEB-2001; 2001GB-0003424.
 PA (CHIR-) CHIRON SPA.
 XX PI Fontana MR, Pizza M, Masignani V, Monaci E;
 XX WPI; 2003-058415/05.
 DR N-PSDB; ABZ3951.
 XX PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection -
 XX PS Disclosure; Page 517; 815pp; English.

Query Match 63.5%; Score 33; DB 22; Length 534;

PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSEQ) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 WPI: 2001-639362/73.
 DR N-PSDB; AAS78648.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX

PS Claim 20; SEQ ID No 44820; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010 ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences.

SQ Sequence 657 AA;

Query	Match	Best Local Similarity	Score	Length
Qy	1 MKQAFVFF 9	63.5%	33; DB 22;	657;
Db	132 MKSAFWFSF 140	66.7%	Pred. No. 2.6e+02;	
		Matches 6;	Mismatches 1;	Indels 0;
				Gaps 0;

Search completed: July 24, 2003, 20:05:57
 Job time : 9.72727 secs

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/971,244
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-971-244-2

Query Match Score 34; DB 2; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 1.3e-02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFYFEFD 10
 Db 1240 LKVLFLEFD 1249

RESULT 3 US-09-286-891-2
 Sequence 2, Application US/09/286891
 Patent No. 6172195
 GENERAL INFORMATION:
 APPLICANT: Cohen, Lucy
 APPLICANT: Bauerle, Patrick
 TITLE OF INVENTION: Icap Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/286,891
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/971,244
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

MOLECULE TYPE: protein

Query Match Score 34; DB 3; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 1.3e-02;

RESULT 4 US-08-286-819A-41
 Sequence 41, Application US/08/286819A
 Patent No. 5871910
 GENERAL INFORMATION:
 APPLICANT: ARTHUR, MICHEL
 APPLICANT: DUKTA-MALLEN, SYLVIE
 APPLICANT: MOLINAS, CATHERINE
 APPLICANT: COURVALIN, PATRICE
 TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE EXPRESSION OF RESISTANCE TO GLYCOPEPITIDES, IN PARTICULAR SEQUENCES IMPLICATED IN THE EXPRESSION OF RESISTANCE TO GLYCOPEPITIDES, IN PARTICULAR
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 21P: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,819A
 FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/174,682
 FILING DATE: 28-DEC-1993
 CLASSIFICATION: 35
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/917,146
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR/91/00855
 FILING DATE: 29-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9013579
 FILING DATE: 31-OCT-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5871910man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 66-0-060-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 243855 OPAT UR
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli

US-08-286-819A-41

Query Match Score 33; DB 2; Length 256;

Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KOAFVFFD 10
Db 123 KOFFFEID 131

RESULT 5
US-08-980-357-41
Sequence 41, Application US/08980357
Patent No. 6013508
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
TITLE OF INVENTION: THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US/08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/917,145
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579f
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Escherichia coli

Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KOAFVFFD 10
Db 123 KOFFFEID 131

RESULT 6
US-09-134-001C-5032
Sequence 5032, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS AUREUS FAECUTUM FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIORITY APPLICATION NUMBER: US 60/064,964
PRIORITY FILING DATE: 1997-11-08
PRIORITY APPLICATION NUMBER: US 60/055,779
PRIORITY FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5032
LENGTH: 218
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5032

Query Match 59.6%; Score 31; DB 4; Length 218;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFVFFD 10
Db 8 MYKAVVFFED 17

RESULT 7
US-09-107-512A-6194
Sequence 6194, Application US/09107532A
Patent No. 6582275
GENERAL INFORMATION:
APPLICANT: Lynn A. Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECUTUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02454
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISS9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107-532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 1-May-1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Denke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:

Query Match 63.5%; Score 33; DB 3; Length 256;

TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 6194:
 SEQUENCE CHARACTERISTICS:
 TYPE: 237 amino acids
 TOPOLogy: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...237
 SEQUENCE DESCRIPTION: SEQ ID NO: 6194 :
 US-09-107-532A-6194

Query Match Score 59.6%; Pred. No. 1.4e+02; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 AFVFEFD 10
 Db 11:1:1
 10 AFLFEYD 16

RESULT 9
 US-09-191-608-22
 ; Sequence 22, Application US/09191608
 ; Patent No. 6242216
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynch, Kevin J.
 ; APPLICANT: Burgard, Edward C.
 ; APPLICANT: Metzger, Randy E.
 ; APPLICANT: Niforatos, Wende
 ; APPLICANT: Touma, Edward B.
 ; APPLICANT: Van Biesen, T.
 ; TITLE OF INVENTION: Nucleic Acids Encoding a Functional
 ; TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
 ; FILE REFERENCE: 6394 US P1
 ; CURRENT APPLICATION NUMBER: US/09/191,608
 ; CURRENT FILING DATE: 1998-11-13
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 22
 ; LENGTH: 388
 ; TYPE: PRY
 ; ORGANISM: Homo sapiens
 US-09-191-608-22

Query Match Score 59.6%; Pred. No. 1.4e+02; Length 388;
 Best Local Similarity 71.4%; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKQAFVFEP 9
 Db 143 MKQAFVFEP 151

RESULT 8
 US-08-742-621-1
 ; Sequence 1, Application US/08742621
 ; Patent No. 5856129
 ; GENERAL INFORMATION:
 ; APPLICANT: HILLMAN, JENNIFER L.
 ; APPLICANT: COLEMAN, ROGER
 ; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/742,621
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 388 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLogy: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: consensus
 ; CLONE: consensus
 Query Match Score 59.6%; Pred. No. 1.4e+02; Length 388;

RESULT 10
 US-08-742-621-3
 ; Sequence 3, Application US/08742621
 ; Patent No. 5856129
 ; GENERAL INFORMATION:
 ; APPLICANT: HILLMAN, JENNIFER L.
 ; APPLICANT: COLEMAN, ROGER
 ; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/742,621
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 388 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLogy: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: consensus
 ; CLONE: consensus
 Query Match Score 59.6%; Pred. No. 1.4e+02; Length 388;

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 PRIORITY/DOCKET NUMBER: PF-0147 US
 PRIORITY INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 PRIORITY/DOCKET NUMBER: PF-0147 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 LENGTH: 399 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 166438
 US-08-742-621-3

Query Match 59.6%; Score 31; DB 2; Length 399;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AFVFEFD 10
 Db 11 AFLFEYD 17

RESULT 12
 US-09-363-745-11
 ; Sequence 11, Application US/09363745
 ; Patent No. 6194162
 ; GENERAL INFORMATION:
 ; APPLICANT: VALERA, SOLEDAD
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLOBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/363-745
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/750,134
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CRAWFORD, ARTHUR C.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 1430-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-0006
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 399 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-363-745-11

Query Match 59.6%; Score 31; DB 3; Length 399;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AFVFEFD 10
 Db 11 AFLFEYD 17

RESULT 13
 US-08-363-134A-11
 ; Sequence 11, Application US/08363134A
 ; Patent No. 5885603
 ; GENERAL INFORMATION:
 ; APPLICANT: BUELL, GARY
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLOBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/750,134A
 ; FILING DATE: 22-JAN-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CRAWFORD, ARTHUR C.
 ; REGISTRATION NUMBER: 25,327
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4006
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 399 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-750-134A-11

Query Match 59.6%; Score 31; DB 2; Length 399;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AFVFEFD 10
 Db 11 AFLFEYD 17

RESULT 14
 US-08-631-607-4
 ; Sequence 4, Application US/08631607
 ; Patent No. 5767252
 ; GENERAL INFORMATION:
 ; APPLICANT: Worley et al., Paul
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA, USA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/631,607
 FILING DATE: 08-APR-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/086001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678 5070
 TELEFAX: 619/678-5099
 SEQUENCE CHARACTERISTICS:
 LENGTH: 211 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-631-607-4

Query Match	57.7%	Score 30;	DB 1;	Length 211;
Best Local Similarity	100.0%	Pred. No.	1.2e+02;	
Matches	6;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 2 KQAFVF 7
 Db 6 KQAFVF 11

RESULT 14
 US-09-098-358B-4
 ; Sequence 4 , Application US/09098358B
 ; Patent No. 6436673

GENERAL INFORMATION:
 ; APPLICANT: THE JOHN HOPKINS SCHOOL OF MEDICINE
 ; APPLICANT: WORLEY, PAUL
 ; APPLICANT: TSUJI, CYNTHIA
 ; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
 ; FILE REFERENCE: JHU 1340-1 (07265/086002)
 ; CURRENT APPLICATION NUMBER: US/09/098,358B
 ; CURRENT FILING DATE: 1998-06-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: ARTIFICIAL
 ; FEATURE:
 ; OTHER INFORMATION: RAT CRP

US-09-098-358B-4

Query Match	57.7%	Score 30;	DB 4;	Length 211;
Best Local Similarity	100.0%	Pred. No.	1.2e+02;	
Matches	6;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 2 KQAFVF 7
 Db 6 KQAFVF 11

RESULT 15
 US-08-906-769-81
 ; Sequence 81 , Application US/08906769
 ; Patent No. 6077687

GENERAL INFORMATION:
 ; APPLICANT: Grieve, Robert B.
 ; APPLICANT: Ruslow, Keith E.
 ; APPLICANT: Wu Hunter, Shirley
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Stiegler, Gary
 ; APPLICANT: Gaines, Patrick J.
 ; APPLICANT: Silver, Gary
 ; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 20:08:50 ; Search time 4.28571 Seconds
 (without alignments)
 277.106 Million cell updates/sec

Title: US-09-546-136-1

Perfect score: 52

Sequence: 1 MKQAFVFFED 10

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 451899 seqs, 11875970 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_ANA:*

1: /cgn2_6/picodata/2/pubpaas/US07_PUBCOMB.pep:*

2: /cgn2_6/picodata/2/pubpaas/PCT_News_Pub.pep:*

3: /cgn2_6/picodata/2/pubpaas/US06_NEw_Pub.pep:*

4: /cgn2_6/picodata/2/pubpaas/US06_PUBCOMB.pep:*

5: /cgn2_6/picodata/2/pubpaas/US07_NEw_Pub.pep:*

6: /cgn2_6/picodata/2/pubpaas/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/picodata/2/pubpaas/US08_NEw_Pub.pep:*

8: /cgn2_6/picodata/2/pubpaas/US08_PUBCOMB.pep:*

9: /cgn2_6/picodata/2/pubpaas/US09_PUBCOMB.pep:*

10: /cgn2_6/picodata/2/pubpaas/US07_NEw_Pub.pep:*

11: /cgn2_6/picodata/2/pubpaas/US09_PUBCOMB.pep:*

12: /cgn2_6/picodata/2/pubpaas/US09_NEw_Pub.pep:*

13: /cgn2_6/picodata/2/pubpaas/US10_PUBCOMB.pep:*

14: /cgn2_6/picodata/2/pubpaas/US10B_PUBCOMB.pep:*

15: /cgn2_6/picodata/2/pubpaas/US10C_PUBCOMB.pep:*

16: /cgn2_6/picodata/2/pubpaas/US10_NEw_Pub.pep:*

17: /cgn2_6/picodata/2/pubpaas/US60_NEw_Pub.pep:*

18: /cgn2_6/picodata/2/pubpaas/US60_PUBCOMB.pep:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	69.2	749	15 US-10-099-352-40	Sequence 40, Appl
2	34	65.4	1332	14 US-10-041-056-3	Sequence 3, Appl
3	34	65.4	1332	14 US-10-041-056-5	Sequence 5, Appl
4	33	63.5	538	11 US-09-820-043A-9	Sequence 9, Appl
5	32	61.5	91	14 US-10-090-035-22	Sequence 22, Appl
6	32	61.5	92	14 US-10-090-035-20	Sequence 20, Appl
7	32	61.5	92	14 US-10-090-035-24	Sequence 24, Appl
8	32	61.5	744	15 US-10-099-352-41	Sequence 41, Appl
9	31	59.6	45	9 US-09-884-761-39890	Sequence 3890, A
10	31	59.6	388	10 US-09-833-082-2	Sequence 2, Appl
11	31	59.6	431	15 US-10-116-761-9506	Sequence 9506, AP
12	30	57.7	88	10 US-09-196-632-995	Sequence 995, AP
13	30	57.7	88	10 US-09-196-592-1524	Sequence 1524, AP
14	30	57.7	88	15 US-10-040-862-995	Sequence 995, AP
15	30	57.7	88	15 US-10-040-862-1524	Sequence 1524, AP

ALIGNMENTS

RESULT 1
 US-10-099-352-40
 ; Sequence 40, Application US-10099152
 ; Publication No. US20030082569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, Clayton H.
 ; ATTORNEY: York, J. Lynda
 ; APPLICANT: McEwen, Joann E.
 ; TITLE OF INVENTION: Histoplasma Capsulation Catalase Sequences and Their Use in t
 ; TITLE OF INVENTION: of Histoplasma Capsulation and Histoplasmosis
 ; FILE REFERENCE: 4071-255988
 ; CURRENT APPLICATION NUMBER: US10/0999, 352
 ; CURRENT FILING DATE: 2002-03-13
 ; PRIORITY APPLICATION NUMBER: US 60/275, 353
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 40
 ; LENGTH: 749
 ; TYPE: PRT
 ; ORGANISM: Aspergillus fumigatus
 US-10-099-352-40

Query Match 8 Best Local Similarity 69.2%; Score 69.2%; DB 15; Length 749;
 Matches 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MKQAFVFFED 10
 Db 487 MKQAFSEFD 496

RESULT 2
 US-10-041-856-3
 ; Sequence 3, Application US/10041856
 ; Publication No. US2002016929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SLAUGENHAUPT, SUSAN

APPLICANT: GUSELLA, JAMES F.
 TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
 FILE REFERENCE: 1829-4004US1
 CURRENT APPLICATION NUMBER: US/10/041,856
 CURRENT FILING DATE: 2002-07-08
 PRIOR APPLICATION NUMBER: 60/260,080
 PRIOR FILING DATE: 2001-01-06
 NUMBER OF SEQ ID NOS: 88
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 1332
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-041-856-3

Query Match 65.4%; Score 34; DB 14; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKQAFVFEFD 10
 Db 1240 LKVLFLEFD 1249

RESULT 3
 US-10-041-856-5
 ; Sequence 5, Application US/10041856
 ; Publication No. US20020169299A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SLAUGENHAUPT, SUSAN
 ; APPLICANT: GUSELLA, JAMES F.
 ; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
 ; FILE REFERENCE: 1829-4004US1
 ; CURRENT APPLICATION NUMBER: US/10/041,856
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/260,080
 ; PRIOR FILING DATE: 2001-01-06
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-041-856-5

Query Match 65.4%; Score 34; DB 14; Length 1332;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKQAFVFEFD 10
 Db 1240 LKVLFLEFD 1249

RESULT 4
 US-09-820-843A-9
 ; Sequence 9, Application US/09820843A
 ; Publication No. US20030039963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Council of Scientific and Industrial Research
 ; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
 ; FILE REFERENCE: Q6315
 ; CURRENT APPLICATION NUMBER: US/09/820,843A
 ; CURRENT FILING DATE: 2001-03-30
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 538
 ; TYPE: PRT
 ; ORGANISM: H. influenzae

FEATURE;
 NAME/KEY: misc_feature
 OTHER INFORMATION: thiamin ABC transporter, permease protein, putative
 NAME/KEY: misc_feature
 OTHER INFORMATION: g11574049
 US-09-820-843A-9
 Query Match 63.5%; Score 33; DB 11; Length 538;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 QAFVFEFD 10
 Db 234 QAILFEFD 241
 RESULT 5
 US-10-090-035-22
 ; Sequence 22, Application US/10090035
 ; Publication No. US20020170089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMMONS, Carl R.
 ; TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
 ; FILE REFERENCE: 35718/242990
 ; CURRENT APPLICATION NUMBER: US/10/090,035
 ; CURRENT FILING DATE: 2002-02-18
 ; PRIOR APPLICATION NUMBER: 60/272,227
 ; PRIOR FILING DATE: 02/28/2001
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 91
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 US-10-090-035-22
 Query Match 61.5%; Score 32; DB 14; Length 91;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKQAFVFEFD 10
 Db 32 WKETVQEFD 41
 RESULT 6
 US-10-090-035-20
 ; Sequence 20, Application US/10090035
 ; Publication No. US20020170089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMMONS, Carl R.
 ; TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
 ; FILE REFERENCE: 35718/242990
 ; CURRENT APPLICATION NUMBER: US/10/090,035
 ; CURRENT FILING DATE: 2002-02-18
 ; PRIOR APPLICATION NUMBER: 60/272,227
 ; PRIOR FILING DATE: 02/28/2001
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 92
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 US-10-090-035-20
 Query Match 61.5%; Score 32; DB 14; Length 92;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKQAFVFEFD 10
 Db 32 WKETVQEFD 41

Db 33 VKETFVQEF D 42

APPLICANT: Chen, Wenshang
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
 FILE REFERENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/964,761
 CURRENT FILING DATE: 2001-05-23
 PRIORITY NUMBER: US 60/180,312
 PRIORITY FILING DATE: 2000-02-04
 PRIORITY APPLICATION NUMBER: US 60/207,456
 PRIORITY FILING DATE: 2000-05-26
 PRIORITY APPLICATION NUMBER: US 09/632,366
 PRIORITY FILING DATE: 2000-08-03
 PRIORITY APPLICATION NUMBER: GB 24263,6
 PRIORITY FILING DATE: 2000-10-04
 PRIORITY APPLICATION NUMBER: US 60/236,359
 PRIORITY FILING DATE: 2000-09-27
 PRIORITY APPLICATION NUMBER: PCT/US01/00666
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00667
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00664
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00669
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00665
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00668
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00663
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00662
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00661
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00670
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: US 60/234,687
 PRIORITY FILING DATE: 2000-09-21
 PRIORITY APPLICATION NUMBER: US 09/608,408
 PRIORITY FILING DATE: 2000-06-30
 PRIORITY APPLICATION NUMBER: US 09/774,203
 PRIORITY FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 4917
 SOFTWARE: Amnomax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 24
 LENGTH: 92
 TYPE: PRT
 ORGANISM: Triticum aestivum
 US-10-090-035-24

Query Match 61.5%; Score 32; DB 14; Length 92;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFVFEFD 10
 Db 33 VKETFVQEF D 42

RESULT 8

US-10-099-352-41
 Sequence 41, Application US/10099352
 Publication No. US20030082569A1
 GENERAL INFORMATION:
 APPLICANT: Johnson, Clayton H.
 APPLICANT: York, J. Lyndal
 APPLICANT: McEwen, Joan E.
 TITLE OF INVENTION: Histoplasma Capsulation Catalase Sequences and Their Use in the
 TITLE OF INVENTION: Histoplasma Capsulation and Histoplasmosis
 FILE REFERENCE: 40715-25988
 CURRENT APPLICATION NUMBER: US/10/099,352
 CURRENT FILING DATE: 2002-03-13
 PRIORITY NUMBER: US 60/275,353
 PRIORITY FILING DATE: 2001-03-13
 NUMBER OF SEQ ID NOS.: 48
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 41
 LENGTH: 744
 TYPE: PRT
 ORGANISM: *Emericella nidulans*
 US-10-099-352-41

Query Match 61.5%; Score 32; DB 15; Length 744;
 Best Local Similarity 60.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKQAFVFEFD 10
 :1:1:1:1:1
 Db 481 VKKAFSEFD 490

RESULT 9

US-09-864-761-39890
 Sequence 39890, Application US/09864761
 Publication No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.

Query Match 59.6%; Score 31; DB 9; Length 45;
 Best Local Similarity 71.4%; Pred. No. 30;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: EST-HUMAN HIT: AU118048.1, EVALUE 4.00e-08
 US-09-864-761-39890

Qy 4 AFLFEYD 10
 :1:1:1:
 Db 11 AFLFEYD 17

RESULT 10
 US-09-833-082-2

```

; Sequence 2, Application US/098333082
; Patent No. US20020151480A1
; GENERAL INFORMATION:
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 10218
; FILE REFERENCE: MNI-227
; CURRENT APPLICATION NUMBER: US/09/833,082
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO: 2
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-833-082-2

Query Match      59.6%;  Score 31;  DB 10;  Length 388;
Best Local Similarity 71.4%;  Pred. No. 2.6e-02;
Matches 5;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;
Prior Filing Date: 2000-04-27
Prior Application Number: 60/190,479
Prior Filing Date: 2000-03-17
Prior Application Number: 60/200,545
Prior Filing Date: 2000-04-28
Prior Application Number: 60/200,779
Prior Filing Date: 2000-04-28
Prior Application Number: 60/200,545
Prior Filing Date: 2000-05-01
Prior Application Number: 60/202,084
Prior Filing Date: 2000-05-04
Prior Application Number: 60/205,201
Prior Filing Date: 2000-05-22
Prior Application Number: 60/218,950
Prior Filing Date: 2000-07-14
Prior Application Number: 60/222,903
Prior Filing Date: 2000-08-03
Prior Application Number: 60/223,416
Prior Filing Date: 2000-08-04
Prior Application Number: 60/223,378
Prior Filing Date: 2000-08-07
Number of SEQ ID NOS: 9597
Software: FastSEQ for Windows Version 4.0
SEQ ID NO 995
Length: 88
TYPE: PRT
ORGANISM: Homo sapiens
US-09-796-692-395

RESULT 13
US-10-156-761-9506
; Sequence 9506, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, JUN
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIOUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-2272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9506
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; US-10-156-761-9506

Query Match      59.6%;  Score 31;  DB 15;  Length 431;
Best Local Similarity 70.0%;  Pred. No. 2.9e-02;
Matches 7;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
Prior Filing Date: 2001-03-01
Prior Application Number: US/09/796,692
Prior Filing Date: 2007-01200
Current Application Number: US/09/796,692
Current Filing Date: 2000-04-27
Prior Application Number: 60/186,126
Prior Filing Date: 2000-04-28
Prior Application Number: 60/190,479
Prior Filing Date: 2000-03-17
Prior Application Number: 60/200,545
Prior Filing Date: 2000-05-01
Prior Application Number: 60/202,084
Prior Filing Date: 2000-05-04
Prior Application Number: 60/206,201
Prior Filing Date: 2000-05-22
Prior Application Number: 60/218,950

RESULT 12
US-09-796-692-995
; Sequence 995, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Aigate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND TREATMENT OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077-001200

Query Match      59.6%;  Score 31;  DB 15;  Length 431;
Best Local Similarity 70.0%;  Pred. No. 2.9e-02;
Matches 7;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
Prior Filing Date: 2000-03-01
Prior Application Number: 60/186,126
Prior Filing Date: 2000-04-28
Prior Application Number: 60/190,479
Prior Filing Date: 2000-03-17
Prior Application Number: 60/200,545
Prior Filing Date: 2000-05-01
Prior Application Number: 60/202,084
Prior Filing Date: 2000-05-04
Prior Application Number: 60/206,201
Prior Filing Date: 2000-05-22
Prior Application Number: 60/218,950

```

```

; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1524
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1524

RESULT 15
Query Match      57.7%; Score 30; DB 15; Length 88;
Best Local Similarity 83.3%; Pred. No. 90; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 5; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Qy      5 FVFEFD 10
Db      62 FMFEFD 67

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; Sequence 95, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1524
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1524

Query Match      57.7%; Score 30; DB 15; Length 88;
Best Local Similarity 83.3%; Pred. No. 90; Mismatches 1; Conservative 5; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 5; Pred. No. 90; Mismatches 1; Conservative 5; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Qy      5 FVFEFD 10
Db      62 FMFEFD 67

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; Sequence 95, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1524
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1524

Query Match      57.7%; Score 30; DB 15; Length 88;
Best Local Similarity 83.3%; Pred. No. 90; Mismatches 1; Conservative 5; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 5; Pred. No. 90; Mismatches 1; Conservative 5; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Qy      5 FVFEFD 10
Db      62 FMFEFD 67

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; Sequence 95, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1524
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1524

Search completed: July 24, 2003, 20:21:00
Job time : 8.28571 secs

```

Result No.	Score	Query Match	Length	DB ID	Description
1	33	63.5	538	5 US-09-820-843B-9	Sequence 9, Appli
2	31	59.6	345	7 US-60-478-106-3285	Sequence 3285, Ap
3	27	51.9	42	6 US-10-573-6148	Sequence 6148, Ap
4	27	51.9	185	1 PCT-US02-20480-34	Sequence 34, Appli
5	27	51.9	315	6 US-10-275-555A-34	Sequence 34, Appli
6	27	51.9	406	1 PCT-US02-41612A-448	Sequence 448, Appli
7	27	51.9	523	6 US-10-451-010-1	Sequence 1, Appli
8	27	51.9	753	7 US-60-479-073-437	Sequence 437, Ap
9	27	51.9	854	6 US-10-273-573-6450	Sequence 6450, Ap
10	27	51.9	906	7 US-60-479-073-177	Sequence 177, Ap
11	27	51.9	906	7 US-60-479-073-178	Sequence 178, Ap
12	27	51.9	933	6 US-10-372-227-35	Sequence 35, Appli
13	26	50.0	15	6 US-10-371-525A-137	Sequence 137, Ap
14	26	50.0	15	6 US-10-371-645-137	Sequence 137, Ap
15	26	50.0	15	6 US-10-371-260-137	Sequence 137, Ap
16	26	50.0	56	6 US-10-273-573-6460	Sequence 6460, Ap
17	26	50.0	307	5 US-09-99-760B-2	Sequence 2, Appli
18	26	50.0	314	6 US-10-331-496A-64	Sequence 64, Appli
19	26	50.0	332	6 US-10-294-433-660	Sequence 660, Ap
20	26	50.0	395	6 US-10-323-069A-128	Sequence 128, Ap
21	26	50.0	501	6 US-10-450-200-3	Sequence 3, Appli
22	25.5	49.0	343	6 US-10-332-176A-2	Sequence 2, Appli
23	25.5	49.0	574	6 US-10-332-176A-6	Sequence 6, Appli
24	25.5	49.0	574	6 US-10-332-176A-8	Sequence 8, Appli
25	25.5	49.0	599	6 US-10-332-176A-10	Sequence 10, Appli
26	25	48.1	130	1 PCT-US03-18448-5	Sequence 5, Appli

```

; LENGTH: 345
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-60-478-196-3285

Query Match      59  6% ; Score 31; DB 7; Length 345;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy   1 MKQAFVFEFD 10
Db  196 LKAAATQYQFD 205

RESULT 3
; Sequence 6148, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 6148
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-273-573-6148

Query Match      59  6% ; Score 31; DB 7; Length 345;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy   1 MKQAFVFEFD 10
Db  196 LKAAATQYQFD 205

RESULT 3
; Sequence 6148, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO: 6148
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-273-573-6148

Query Match      59  6% ; Score 31; DB 7; Length 345;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy   1 MKQAFVFEFD 10
Db  196 LKAAATQYQFD 205

RESULT 4
; Sequence 34. Application PC/TUS0320480
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: ELLIOTT, Vick S.
; APPLICANT: MASON, Patricia M.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: LEE, Soo Yuen
; APPLICANT: RAMKUMAR, Jayalakshmi
; APPLICANT: KABLE, Amy E.
; APPLICANT: SWARNAKAR, Anita
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: HAFLAJA, April J.A.
; APPLICANT: KHARE, Reena
; APPLICANT: BECHA, Shanya D.
; APPLICANT: MAROIS, Joseph P.
; APPLICANT: CHIEN, David
; APPLICANT: JIN, Pei
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: BULLOCH, Sean A.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: ENZYMEs
; FILE REFERENCE: PF-1452_PCT
; CURRENT APPLICATION NUMBER: PCT/US03/20480
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US 60/393,067
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PERL Program
; SEQ ID NO: 34
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 3035248CD1
; US-10-275-595A-34

Query Match      51  9% ; Score 27; DB 1; Length 185;
; Best Local Similarity 51.1%; Pred. No. 33;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
; LOCATION: (1) ... (185)
; OTHER INFORMATION: unknown or other
PCT-US03-20480-34

Query Match      51  9% ; Score 27; DB 1; Length 185;
; Best Local Similarity 51.1%; Pred. No. 33;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
; LOCATION: (1) ... (185)
; OTHER INFORMATION: unknown or other
PCT-US03-20480-34

RESULT 5
; Sequence 34, Application US/10275595A
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dzung Aina M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LAL, Preeti
; APPLICANT: YAO, Monique G.
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neill
; APPLICANT: BATRA, Sajeet
; APPLICANT: KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: POLICKY, Jennifer L.
; TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0772_USN
; CURRENT APPLICATION NUMBER: US/10/275,595A
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/201,960
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/202,729
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 60/209,705
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/210,149
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,215
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PERL Program
; SEQ ID NO: 34
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 3035248CD1
; US-10-275-595A-34

Query Match      51  9% ; Score 27; DB 6; Length 315;
; Best Local Similarity 62.5%; Pred. No. 60;
; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; LOCATION: (1) ... (315)
; OTHER INFORMATION: unknown or other
PCT-US03-20480-34

```

Qy 1 MKQAFVFE 8
 Db :1:111 |
 193 LKEAFVFE 200

RESULT 6
 PCT-US02-41612A-448
 ; Sequence 448, Application PC/TUS0241612A
 ; GENERAL INFORMATION:
 ; APPLICANT: Diadexus, Inc.
 ; APPLICANT: Sun, Yongming
 ; APPLICANT: Liu, Chenghua
 ; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes
 ; FILE REFERENCE: DEX-0378
 ; CURRENT APPLICATION NUMBER: PCT/US02/41612A
 ; CURRENT FILING DATE: 2003-06-17
 ; PRIOR APPLICATION NUMBER: 60/342,756
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 600
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 448
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapien

PCT-US02-41612A-448

Query Match Score 27; DB 1; Length 406;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AFVFEF 9
 Db :1:111 11 AFAFEF 16

RESULT 7
 US-10-451-010-1
 ; Sequence 1, Application US/10451010
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: DUGGAN, Brendan M.
 ; APPLICANT: XU, Yuming
 ; APPLICANT: LEE, Ernestine A.
 ; APPLICANT: LEE, Sally
 ; APPLICANT: LU, Dyoung Aina M.
 ; APPLICANT: WARREN, Bridget A.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: GIETZEN, Kimberly J.
 ; APPLICANT: HONCHELL, Cynthia D.
 ; APPLICANT: BURFORD, Neil
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: JACKSON, Jennifer L.
 ; APPLICANT: GANDHI, Aneena R.
 ; APPLICANT: KALLICK, Deborah A.
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: GRAUL, Richard C.
 ; APPLICANT: CHAWLA, Narinder K.
 ; APPLICANT: LU, Yan
 ; APPLICANT: RAMKOUR, Jayalaxmi
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: LAL, Freeli G.
 ; TITLE OF INVENTION: CELL ADHESION PROTEINS
 ; FILE REFERENCE: P-0867, USN
 ; CURRENT APPLICATION NUMBER: US/10/451,010
 ; CURRENT FILING DATE: 2003-06-17
 ; PRIOR APPLICATION NUMBER: PCT/US01/49206
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: US 60/256,542
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: US 60/259,604
 ; PRIOR FILING DATE: 2000-12-22

Query Match Score 27; DB 6; Length 523;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KOAFVFEF 9
 Db :1:111 11
 482 EQAFLVEF 489

RESULT 8
 US-60-479-073-437
 ; Sequence 437, Application US/60479073
 ; GENERAL INFORMATION:
 ; APPLICANT: De Wilde, Gert Jules Hector
 ; APPLICANT: Saunders, Michael John Scott
 ; APPLICANT: Logghe, Marc Georges
 ; TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the prevention and/or treatment of metabolic diseases and nuclear

Qy 2 KOAFVFEF 9
 Db :1:111 11
 482 EQAFLVEF 489

Query Match Score 27; DB 7; Length 753;
 Best Local Similarity 50.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KOAFVFEF 9
 Db :1:111 11
 737 KEGFTFEY 744

RESULT 9
 US-10-273-573-6450
 ; Sequence 6450, Application US/10273573
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 21272-066
 ; CURRENT APPLICATION NUMBER: US/10/273,573
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 09/522,929
 ; PRIOR FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: 09/770,160
 ; PRIOR FILING DATE: 2001-01-26
 ; NUMBER OF SEQ ID NOS: 10994
 ; SEQ ID NO: 6450
 ; SOFTWARE: Custom
 ; LENGTH: 854
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: DOMAIN
 ; NAME/KEY: DOMAIN

LOCATION: (431)..(481)
; OTHER INFORMATION: Eukaryotic DNA topoisomerase I proteins domain identified by BL00176A, accession number BL00176A, p-value=1.000e-40, raw score 28.37
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (204)..(854)
; OTHER INFORMATION: Eukaryotic DNA topoisomerase I domain identified by PFam, accession name 'topoisomerase_I', E-value=0, PFam score of 1431.8
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(854)
; OTHER INFORMATION: Xaa - X or * as defined in Table 2
US-10-273-6450

Query Match Score 27; DB 6; Length 854;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QAFVFFED 10
Db 609 QEXVWEED 616

RESULT 10
US-60-479-073-177
; Sequence 177, Application US/60479073.
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Gert Jules Hector
; APPLICANT: Saunders, Michael John Scott
; APPLICANT: Logue, Marc Georges
; TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the prevention and/or treatment of metabolic diseases and nucleotide sequences encoding such amino acid sequences.
; FILE REFERENCE: D00590 70042.US
; CURRENT APPLICATION NUMBER: US/60/479,073
; CURRENT FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: PatentIn version 3.2
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 177

Query Match Score 27; DB 7; Length 906;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKQAFVFE 8
Db 801 LKEAFVFE 808

RESULT 11
US-60-479-073-178
; Sequence 178, Application US/60479073.
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Gert Jules Hector
; APPLICANT: Saunders, Michael John Scott
; APPLICANT: Logue, Marc Georges
; TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the prevention and/or treatment of metabolic diseases and nucleotide sequences encoding such amino acid sequences.
; FILE REFERENCE: D00590 70042.US
; CURRENT APPLICATION NUMBER: US/60/479,073
; CURRENT FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 178
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match Score 27; DB 7; Length 906;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKQAFVFE 8
Db 801 LKEAFVFE 808

RESULT 12
US-10-372-227-35
; Sequence 35, Application US/10372227.
; GENERAL INFORMATION:
; APPLICANT: Hitachi, Ltd.
; TITLE OF INVENTION: OPAL-INTERACTING PROTEINS AND USE THEREOF
; FILE REFERENCE: HITA-0168
; CURRENT APPLICATION NUMBER: US/10/372,227
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,374
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US 60/407,247
; PRIOR FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 35
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-227-35

Query Match Score 27; DB 6; Length 933;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQAFVF 7
Db 824 RQAFVF 829

RESULT 13
US-10-371-525A-137
; Sequence 137, Application US/10371525A.
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; Fikes, John D.
; Hermanson, Gary G.
; Sette, Alessandro
; Ishioka, Glenn Y.
; Livingston, Brian
; Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.12
; CURRENT APPLICATION NUMBER: US/10/371,525A
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 137
; LENGTH: 15
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: HBV POL 661 (peptide 1298.06)
US-10-371-525A-137

Query Match Score 26; DB 6; Length 15;

Best Local Similarity 83.3%; Pred. No. 3.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KQAFVF 7
Db 1 KQAFTE 6

RESULT 14
US-10-371-645-137
Sequence 137, Application US/10371645
GENERAL INFORMATION:
APPLICANT: EPIMMUNE Inc.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.11

CURRENT APPLICATION NUMBER: US/10/371,645
PRIORITY FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 137
LENGTH: 15

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBV POL 661 (peptide 1298.06)
US-10-371-645-137

Query Match 50.0%; Score 26; DB 6; Length 15;
Best Local Similarity 83.3%; Pred. No. 3.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KQAFVF 7
Db 1 KQAFTE 6

RESULT 15
US-10-371-260-137
Sequence 137, Application US/10371260
GENERAL INFORMATION:
APPLICANT: EPIMMUNE Inc.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.13
CURRENT APPLICATION NUMBER: US/10/371,260
PRIORITY FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 137
LENGTH: 15

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

CM protein - protein search, using sw model

Run on: July 24, 2003, 20:04:00 ; Search time 3.24675 Seconds

(without alignments)
296.200 Million cell updates/sec

Title: US-09-546-136-1

Perfect score: 52

Sequence: 1 MKQAFVFEFD 10

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	69.2	271	2 JQ2285	nodulin-26 - soybean
2	36	69.2	271	2 JQ2286	nodulin-26 - soybean
3	36	69.2	271	2 S01444	nodulin-26 precursor
4	34	65.4	285	2 B90445	regucalcin homolog
5	34	65.4	285	2 T08677	hypothetical protein
6	33	63.5	431	1 RGEFCFR	sensor kinase (EC
7	33	63.5	431	2 B44753	sensor kinase (EC
8	33	63.5	431	2 B90682	hypothetical protein
9	33	63.5	431	2 F85535	hypothetical protein
10	33	63.5	538	1 D64164	hypothetical protein
11	33	63.5	538	2 F84648	hypothetical protein
12	32	61.5	45	2 PC4177	phosphoglycolate P
13	32	61.5	84	2 A27144	larval serum prote
14	32	61.5	100	1 B27144	hypothetical protein
15	32	61.5	141	1 H69385	probable signal pe
16	32	61.5	167	2 T37486	probable peptidogl
17	32	61.5	188	2 E71495	peptidoglycan asso
18	32	61.5	202	2 G81653	hypothetical protein
19	32	61.5	371	2 T49786	hypothetical protein
20	32	61.5	395	1 F64351	ABC transporter (m
21	32	61.5	408	2 G69619	T1K7.21 protein -
22	32	61.5	552	2 H86390	catalase (EC 1.1.1.
23	32	61.5	744	2 S68115	phenylalanine-tRNA
24	32	61.5	804	1 YFB5B	carbon-monoxide de
25	32	61.5	842	2 S49124	probable bacteriop
26	31	59.6	124	2 AC0803	hypothetical protein
27	31	59.6	230	2 F71122	hypothetical protein
28	31	59.6	283	2 S64347	hypothetical protein
29	31	59.6	329	2 D96834	hypothetical protein

30	31	59.6	368	2 T27432	hypothetical protein
31	31	59.6	385	2 T23065	hypothetical protein
32	31	59.6	396	2 E70233	ARP-gated ion chan
33	31	59.6	399	2 S71927	hypothetical prote
34	31	59.6	439	2 T45798	probable copper-co
35	31	59.6	445	2 T3366	hypothetical prote
36	31	59.6	449	2 C93332	multicopper oxida
37	31	59.6	449	2 A98239	probable transport
38	31	59.6	449	2 AC1047	probable transport
39	31	59.6	456	1 C64772	probable transport
40	31	59.6	456	1 A90989	probable transport
41	31	59.6	456	2 E85539	hypothetical prote
42	31	59.6	459	2 T10307	peptidyl-prolyl ci
43	31	59.6	471	1 S62590	hypothetical dna b
44	31	59.6	569	2 T38627	conserved hypothet
45	31	59.6	587	2 T02829	

ALIGNMENTS

RESULT 1	JQ2285	nodulin-26 - soybean	C; Species: Glycine max (soybean)
			C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999
			C; Accession: JQ2285
			R:Miao, G.H.; Verma, D.P.S.
			Plant Cell 5, 791-794, 1993
			A:Title: soybean nodulin-26 gene encoding a channel protein is expressed only in the
			A:Reference number: JQ2285; MUID:93372569; PMID:7689881
			A:Accession: JQ2285
			A: Molecule type: DNA
			A: Residues: 1-271 <M1>
			C:Comment: The protein is a major peribacteroid membrane protein in soybean root nuc
			C:Genetics: nodulin-26
			C:Introns: 39/3; 114/3; 180/3; 201/2
			C:Superfamily: nodulin-26
			C:Keywords: transmembrane protein
			F: 40-60/Domain: transmembrane #status predicted <TM1>
			F: 67-88/Domain: transmembrane #status predicted <TM2>
			F: 115-133/Domain: transmembrane #status predicted <TM3>
			F: 156-175/Domain: transmembrane #status predicted <TM4>
			F: 183-203/Domain: transmembrane #status predicted <TM5>
			F: 227-244/Domain: transmembrane #status predicted <TM6>
			Query Match 69.2% Score 36; DB 2; Length 271;
			Best Local Similarity 100.0%; Pred. No. 9.9%; Mismatches 0; Indels 0; Gaps 0;
			Matches 7; Conservative 7;
Qy	3 QAFVFF 9	111111	
		155 QAFVFF 161	
Db			

Query Match 69.2%; Score 36; DB 2; Length 271;
 Best Local Similarity 100.0%; Pred. No. 9.9; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

RESULT 5
 hypothetical protein DKFZP564G2222.1 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
 C;Accession: T08677
 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A;Reference number: Z16469
 A;Accession: T08677
 A;Molecule type: mRNA
 A;Residues: 1-339 <WAM>
 A;Cross-references: EMBL:AL049945
 A;Experimental source: fetal brain; clone DKFZP564G2222
 C;Genetics:
 A;Note: DKFZP564G2222.1

Query Match 65.4%; Score 34; DB 2; Length 339;
 Best Local Similarity 60.0%; Pred. No. 31; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 6; Conservative 6;

RESULT 3
 nodulin-26 precursor - soybean
 C;Species: Glycine max (soybean)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 17-Nov-2000
 C;Accession: S01444; A26445
 R;Sandal, N.N.; Marcker, K.A.
 Nucleic Acids Res. 16, 9347, 1988
 A;Title: Soybean nodulin 26 is homologous to the major intrinsic protein of the bovine 1
 A;Reference number: S01444; MUID:89016643; PMID:3174457
 A;Accession: S01444
 A;Molecule type: mRNA
 A;Residues: 1-271 <SAN>
 A;Cross-references: EMBL:X12659
 R;Fortin, M.G.; Morrison, N.A.; Verma, D.P.S.
 Nucleic Acids Res. 15, 813-824, 1987
 A;Title: Nodulin-26, a peribacteroid membrane nodulin is expressed independently of the 1
 A;Reference number: A26445; MUID:87146395; PMID:3822816
 A;Accession: A26445
 A;Molecule type: mRNA
 A;Residues: 67-271 <FOR>
 A;Experimental source: seed, cv. Prize
 C;Superfamily: nodulin-26
 C;Keywords: phosphoprotein; transmembrane protein

Query Match 69.2%; Score 36; DB 2; Length 271;
 Best Local Similarity 100.0%; Pred. No. 9.9; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

RESULT 4
 regucalcin homolog (imported) - *Sulfolobus solfataricus*
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
 C;Accession: B90445
 R;She, O.; Singh, R.K.; Confolontieri, F.; Zivanovic, Y.; Allard, G.; Ayavez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozaera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arret, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A;Description: *Sulfolobus solfataricus* complete genome.
 A;Reference number: A99139
 A;Accession: B90445
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-285 <KUR>
 A;Cross-references: GB:AE006641; NID:913816023; PIDN:AAK42817.1; GSPDB:GN00155
 C;Genetics:
 A;Gene: SS02705
 C;Superfamily: senscence marker protein-30

Query Match 65.4%; Score 34; DB 2; Length 285;
 Best Local Similarity 50.0%; Pred. No. 26; 4; Mismatches 1; Indels 0; Gaps 0;
 Matches 5; Conservative 5;

RESULT 6
 RGECFR
 sensor kinase (EC 2.7.3.-) phoR - *Escherichia coli* (strain K-12)
 N;Alternate names: phosphate regulon sensor protein phoR
 C;Species: *Escherichia coli*
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 01-Mar-2002
 C;Accession: A25557; H6768; S11888
 R;Makino, K.; Shinagawa, H.; Amemura, M.; Nakata, A.
 J. Mol. Biol. 192, 549-556, 1986
 A;Title: Nucleotide sequence of the phoR gene, a regulatory gene for the phosphate 1
 A;Reference number: A25557; MUID:87169739; PMID:3550103
 A;Accession: A25557
 A;Molecule type: DNA
 A;Residues: 1-431 <MAK>
 A;Cross-references: GB:X04704; NID:942393; PIDN:CAA28409.1; PID:9581188
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:978503
 A;Accession: H64768
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-431 <BLAT>
 A;Cross-references: GB:AB00146; GB:000096; NID:91786596; PIDN: AAC73503.1; PID:9176
 A;Experimental source: strain K-12, substrate MG1655
 R;Yanada, M.; Makino, K.; Shinagawa, H.; Nakata, A.
 Mol. Gen. Genet. 220, 366-372, 1990
 A;Title: Regulation of the phosphate regulon of *Escherichia coli*: properties of pho 1
 A;Reference number: S11888; MUID:90251245; PMID:2187152
 A;Accession: S11888
 A;Molecule type: DNA
 A;Residues: 1-13 <YAM>
 C;Genetics:
 A;Gene: phoR
 A;Map position: 9 min
 A;Start codon: GTG
 C;Function:
 A;Description: transcription regulation; involved in transcription activation of the
 A;Note: phosphorylated phoR protein phosphorylates phoB protein; phosphorylated pho
 C;Superfamily: phosphate regulon regulatory protein; sensor histidine kinase homolog
 C;Keywords: autophosphorylation; membrane protein; phosphate transport; phosphohist
 F:10-26/Domain: transmembrane #status predicted <TM1>
 F:28-44/Domain: transmembrane #status predicted <TM2>
 F:166-422/Domain: sensor histidine kinase homology #status predicted <SHK>
 F:213/Binding site: phosphate (His) (covalent) #status predicted

F; 213/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 63.5%; Score 33; DB 1; Length 431;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Consistency 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 KOAFVFED 10
 Db 298 KOTFFEID 306

RESULT 7

B44753 Sensor kinase (EC 2.7.3.-) phoR - Shigella dysenteriae

C; Species: *Shigella dysenteriae*

C; Accession: BA4753

P; Lee, T.Y.; Makino, K.; Shinagawa, H.; Amemura, M.; Nakata, A.

J; Bacteriol. 171, 6593-6599, 1989

A; Title: Phosphate regulon in members of the family Enterobacteriaceae: comparison of th

A; Reference number: A44753; PMID:90078103; PMID:2556368

A; Status: Preliminary

A; Molecule type: DNA

A; Residues: 1-431 <IEE>

A; Cross-references: EMBL:M31793; PIDN:AAA26536_1; PID:g294893

A; Note: the authors translated the codon CGC for residue 239 as Ala

C; Superfamily: phosphotransferase regulon

C; Keywords: autophosphorylation; phosphotransferase; sensor histidine kinase homology

F; 186-42/Domain: sensor histidine kinase homology <SHK>

F; 213/Binding site: Phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 63.5%; Score 33; DB 2; Length 431;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Consistency 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 KOAFVFED 10
 Db 298 KOTFFEID 306

RESULT 8

B90685 Hypothetical protein ECS0450 [imported] - Escherichia coli (strain O157:H7, substrate R)

C; Species: *Escherichia coli*

C; Accession: B90685

P; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Yokoyama, K.; Han, C.G.

DNA Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno

A; Reference number: A99629; PMID:21156231; PMID:11258796

A; Accession: B90685

A; Status: Preliminary

A; Molecule type: DNA

A; Residues: 1-431 <HAY>

A; Cross-references: GB:BA000007; PIDN:BAE33873_1; PID:g13359907; GSPDB:GN00154

A; Experimental source: strain O157:H7, substrate RIMD 0509952

C; Genetics:

A; Gene: EC0450

C; Superfamily: phosphotransferase regulon

C; Keywords: autophosphorylation; sensor histidine kinase homology

F; 186-42/Domain: sensor histidine kinase homology <SHK>

F; 213/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 63.5%; Score 33; DB 2; Length 431;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Consistency 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 KOAFVFED 10
 Db 298 KOTFFEID 306

RESULT 9

F85535

hypothetical protein phoR [imported] - *Escherichia coli* (strain O157:H7, substrate EC; Species: *Escherichia coli*

C; Accession: F85535

P; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.L.; Ma

iller, L.; Grotter, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potanousis, K.; Apod

A; Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: F85535

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-411 <STO>

A; Cross-references: GB:AE005174; PIDN:g12513246; PIDN:AG54746_1; GSPDB:GN00145; UWGF

A; Experimental source: strain O157:H7, substrate EDL933

C; Genetics:

A; Gene: phoR

C; Superfamily: phosphate regulon regulatory protein; sensor histidine kinase homolog

F; 186-42/Domain: sensor histidine kinase homology <SHK>

F; 213/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 63.5%; Score 33; DB 2; Length 431;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Consistency 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 KOAFVFED 10
 Db 298 KOTFFEID 306

RESULT 10

D64164 Hypothetical protein H11020 - *Haemophilus influenzae* (strain Rd Kw20)C; Species: *Haemophilus influenzae*

C; Accession: D64164

P; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

R.; Gooley, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman

D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.; R.

Science 269, 496-512, 1995

A; Authors: Gnehn, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vent

A; Title: Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A; Reference number: A64000; MUID:9550630; PMID:7542800

A; Accession: D64164

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-538 <TIGR>

A; Cross-references: GB:U32782; GB:L42023; PIDN:91574041; PIDN: AAC22679_1; PID:9157404

A; Note: best homolog was a hypothetical protein from *Escherichia coli*

C; Superfamily: sfbA protein

Query Match 63.5%; Score 33; DB 1; Length 538;
 Best Local Similarity 75.0%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 QAFVFED 10
 Db 234 QAIIFFEFD 241

RESULT 11

F84648 Hypothetical protein At2g25460 [imported] - *Arabidopsis thaliana*C; Species: *Arabidopsis thaliana* (mouse-ear cress)

C; Accession: F84648

P; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Koo, R.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallor

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente

Nature 402, 761-768, 1999

A; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: F84648

A; Status: preliminary

A; Molecule type: DNA

A;Residues: 1-555 <STO>
 A;Cross-references: GB:AE002093; NID:94432857; PMID:AAD20705.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g25460
 A;Map position: 2
 Query Match 63.5%; Score 33; DB 2; Length 555;
 Best Local Similarity 55.6%; Pred. No. 82;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 KOAFVFFFD 10
 Db 476 KOAYILKFD 484

RESULT 12

PC4177

Phosphoglycolate phosphatase (EC 3.1.3.18) - *Synechococcus* sp. (fragment)C;Species: *Synechococcus* sp.

C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 07-May-1999

R:Liu, Y.; Tsiorvas, N.F.

Gene 172, 105-109, 1996

A;Title: An unusual gene arrangement for the putative chromosome replication origin and

A;Reference number: PC4177; PMID:9625762; PMID:8654968

A;Contents: PCC794.2

A;Accession: PC4177

A;Molecule type: DNA

A;Residues: 1-45 <LIU>

A;Cross-references: GB:U333322

C;Genetics:

A;Start codon: TTG

C;Keywords: phosphoric monoester hydrolase

Query Match 61.5%; Score 32; DB 2; Length 45;
 Best Local Similarity 62.5%; Pred. No. 10;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 QAFVFFFD 10
 Db 2 QAIIFDFD 9

RESULT 13

A27144

larval serum protein 1 alpha chain precursor - fruit fly (*Drosophila melanogaster*) (frag)C;Species: *Drosophila melanogaster*

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 21-Jun-2002

C;Accession: A27144

R:Mol. Biol. 189, 1-11, 1986

A;Title: Sequence conservation around the 5' ends of the larval serum protein 1 genes of

A;Reference number: A92926; PMID:87060914; PMID:3097321

A;Accession: A27144

A;Molecule type: DNA

A;Residues: 1-84

C;Genetics:

A;Gene: FlyBase:Lsp1-alpha

A;Cross-references: FlyBase:FBgn0002562

C;Superfamily: arylphorin

Query Match 61.5%; Score 32; DB 2; Length 84;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MKQAFVFE 8
 Db 34 MKQKFLFE 41

B27144

Query Match 61.5%; Score 32; DB 2; Length 100;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MKQAFVFE 8
 Db 34 MKQKFLFE 41Search completed: July 24, 2003, 20:10:22
 Job time : 6.24675 secs

larval serum protein 1 beta chain precursor - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 21-Jun-2002
 C;Accession: B27144
 R:Delaney, S.J.; Smith, D.F.; McClelland, A.; Sunkel, C.; Glover, D.M.
 J. Mol. Biol. 189, 1-11, 1986
 A;Title: Sequence conservation around the 5' ends of the larval serum protein 1 genes of
 A;Reference number: A92926; PMID:87060914; PMID:3097321
 A;Molecule type: DNA
 A;Residues: 1-100
 A;Cross-references: GB:X03873; NID:98193; PMID:CAA27507.1; PID:98194
 C;Genetics:
 A;Gene: FlyBase:Lsp1-beta
 A;Cross-references: FlyBase:FBgn0002563
 C;Superfamily: arylphorin

RESULT 15

H69385

hypothetical protein AF1089 - *Archaeoglobus fulgidus*

C;Species: *Archaeoglobus fulgidus*

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C;Accession: H69385

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; T

; Fleischmann, R.D.; Quackenbush, J.; Lee, M.H.; Sutton, G.G.; Gill, S.; Kirkness, E

; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Ariiach, P.; Kaine, B.P.; Syke

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing ar

A;Reference number: A69220; PMID:9804943; PMID:9389475

A;Accession: H69385

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-141 <KLE>

C;Cross-references: GB:AE001028; GB:AE000782; NID:92689351

C;Superfamily: *Archaeoglobus fulgidus* conserved hypothetical protein AF1711; PID:92689351

Query Match 61.5%; Score 32; DB 1; Length 141;
 Best Local Similarity 83.3%; Pred. No. 33;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVFFFD 10
 Db 14 FIFERD 19

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

CM protein - protein search, using sw model

Run on: July 24, 2003, 19:47:29 ; Search time 1.75325 Seconds
 (without alignments)

268.226 Million cell updates/sec

Title: US-09-546-136-1

Perfect score: 52

Sequence: 1 MKQAFVFEFD 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	36	69.2	271	1	NO26_SOYBN	P09995 glycine max
2	36	69.2	749	1	CATA_ASPPU	P78574 aspergillus
3	34	65.4	1332	1	IKAP_HUMAN	O95163 homo sapien
4	33	63.5	431	1	PHOR_ECOLI	P08400 escherichia
5	33	63.5	431	1	PHOR_SHIDYI	P45609 shigella dysenteriae
6	33	63.5	538	1	THIP_HAEIN	P44985 haemophilus
7	32	61.5	212	1	GPH_SNPI7	Q55039 synchococcus
8	32	61.5	395	1	Y414_METJA	Q57857 methanococcus
9	32	61.5	408	1	ECSB_BACSU	P55340 bacillus su
10	32	61.5	744	1	CATA_EMENI	P55305 americicilia
11	32	61.5	789	1	LP1A_DROME	P11995 drosophila
12	32	61.5	804	1	LP1B_BROME	P11996 drosophila
13	32	61.5	804	1	SYFB_BACSU	P17922 bacillus su
14	32	61.5	1297	1	PUR4_PASMU	P9clv4 pasteurella
15	31	59.6	283	1	YG21_YEAST	P53234 saccharomyces
16	31	59.6	368	1	THII_SULFOB	Q96y5 sulfolobus
17	31	59.6	388	1	P2X4_HUMAN	O95957 homo sapien
18	31	59.6	399	1	P2X1_HUMAN	P51575 homo sapien
19	31	59.6	454	1	YAJR_ECOLI	P77726 escherichia
20	31	59.6	459	1	Y030_NEVOP	O10293 oryza pseu
21	31	59.6	471	1	YAL5_SCHPO	Q09928 schizosacch
22	31	59.6	548	1	SYE_THEVO	Q979q0 thermoplasm
23	31	59.6	2561	1	PPS1_BACSU	P39845 bacillus su
24	30	57.7	127	1	CB1W_BACME	O87688 bacillus me
25	30	57.7	220	1	YHCW_BACSU	P54607 bacillus su
26	30	57.7	230	1	CRP_RAT	P48199 ratus norvegicus
27	30	57.7	241	1	KDKA_HAEIN	O86224 haemophilus
28	30	57.7	260	1	HA2Q_HUMAN	P2036 homo sapien
29	30	57.7	396	1	YC44_CVACA	O19913 cyanidium c
30	30	57.7	408	1	MTV1_VIBS3	Q03055 vibrio sp.
31	30	57.7	419	1	SECY_PAVLU	P23351 neurospora
32	30	57.7	426	1	RMS5_NEUCCR	P23350 pavlovskia
33	30	57.7	452	1	PLM1_PLAFA	P39898 plasmodium

ALIGNMENTS

RESULT 1						
ID	NO26_SOYBN	STANDARD;	PRT;	271 AA.		
AC	P08995;					
DT	01-NOV-1988 (Rel. 09, Created)					
DT	01-FEB-1996 (Rel. 33, Last sequence update)					
DT	30-MAY-2000 (Rel. 39, Last annotation update)					
DE	Nodulin-26 (N-26).					
OS	Glycine max (Soybean).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Ochromelidaceae; Malpighiales; Malpighiidae; Malpighiaceae; Malpighiales; OX					
OC	NCBI_TaxID=3847;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CV Evans;					
RX	MEDLINE=89016643; PubMed=3174457;					
RA	Sandai N.N.; Marcker K.A.;					
RT	"Soybean nodulin 26 is homologous to the major intrinsic protein of the bovine lens fiber membrane."					
RL	the bovine lens fiber membrane;					
RN	[2]					
RP	SEQUENCE OF 67-271 FROM N.A.					
RC	STRAIN=CV; PRIZE;					
RX	MEDLINE=87146395; PubMed=38228116;					
RA	Fortin M.G.; Morrison N.A.; Verma D.P.S.;					
RT	"Nodulin-26, a peribacteroid membrane nodulin is expressed independently of the development of the peribacteroid compartment".					
RL	RT					
RN	[3]					
RP	REVISIONS TO 184 AND 257.					
RC	STRAIN=CV; PRIZE;					
RA	Miao G.H.;					
RL	Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.					
RN	[4]					
RP	PHOSPHORYLATION BY CDPK.					
RX	MEDLINE=93003032; PubMed=1390682;					
RA	Waever C.D.; Roberts D.M.;					
RT	Determination of the site of phosphorylation of nodulin 26 by the calcium-dependent protein kinase from soybean nodules.";					
RL	Biochemistry 31:8954-8959(1992).					
CC	-!- FUNCTION: NOT KNOWN, MAY FUNCTION IN TRANSPORTING SMALL MOLECULES ACROSS THE PERIBACTEROID MEMBRANES (BY SIMILARITY).					
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PERIBACTEROID MEMBRANE.					
CC	-!- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM INFECTION.					
CC	-!- SIMILARITY: BELONGS TO THE MIP/AQUAPORTIN FAMILY (TC 1.A.8).					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					

CC	---	---	Qy	1 MKQATVPEFD 10
DR	EMBL; X04782; CAA28471.1; -.	DR	1 :	
DR	EMBL; X12659; CAA31186.1; -.	DR	487 NKKAFSFELD 496	
DR	HSSP; P1124; 1FX8.			
DR	InterPro; IPR00425; MIP_family.			
DR	Pfam; PF00230; MIP; 1.			
DR	PRINTS; PRO00783; MINTRINSTCP.			
DR	prodBm; PD00029; MIP_FAMILY; 1.			
DR	TIGRFAMS; TIGR00861; MIP; 1.			
DR	PROSITE; PS00221; MIP; 1.			
KW	Nodulation; Nitrogen fixation; Transmembrane; Phosphorylation.			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
FT	TRANSHEM 154			
FT	MOD_RES 262			
SO	SEQUENCE 271 AA; 28935 MW; EA323421D3904284 CRC64;			
Query Match	Score 69.2%; Score 36; DB 1; Length 271;			
Best Local Similarity	100.0%; Pred. No. 7;			
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	3 QAFVFEEF 9			
Db	155 QAFVFEEF 161			
RESULT 2	CATA_ASFPFU STANDARD; PRT; 749 AA.			
ID	CATA_ASFPFU			
AC	P78574;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-FEB-2003 (Rel. 41, Last annotation update)			
DE	Catalase A (EC 1.11.1.6).			
GN	CATA.			
OS	Aspergillus fumigatus (Sartorya fumigata).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillales.			
OX	NCBI_TAXID=5085;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wyson D.R., Diamond R.D., Robbins P.W.; Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.			
RL	FUNCTION: Occurs in almost all aerobically respiring organisms and serves to protect cells from the toxic effects of hydrogen peroxide.			
CC	-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.			
CC	-!- COFACTOR: HEME GROUP.			
CC	-!- SIMILARITY: Belongs to the catalase family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U87630; AAB47761.1; -.			
DR	HSSP; P21179; ICF9.			
DR	InterPro; IPR002226; Catalase.			
DR	Pfam; PF00199; catalase; 1.			
DR	PRINTS; PRO0067; CARALASE.			
DR	prodBm; PD000510; Catalase; 1.			
DR	PROSITE; PS00437; CATALASE_1; 1.			
DR	Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.			
KW	PS00438; CATALASE_2; 1.			
FT	ACT_SITE 93 93 BY SIMILARITY.			
FT	ACT_SITE 166 166 BY SIMILARITY.			
FT	METAL 380 380 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).			
SQ	SEQUENCE 749 AA; 84550 MW; 293854CFB4C826E0 CRC64			
Query Match	Score 69.2%; Score 36; DB 1; Length 749;			
Best Local Similarity	70.0%; Pred. No. 18;			
Matches	7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR HSSP; P21179; ICF9.

DR InterPro; IPR002226; Catalase.

DR Pfam; PF00199; catalase; 1.

DR PRINTS; PRO0067; CARALASE.

DR prodBm; PD000510; Catalase; 1.

DR PROSITE; PS00437; CATALASE_1; 1.

DR Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.

KW PS00438; CATALASE_2; 1.

FT ACT_SITE 93 93 BY SIMILARITY.

FT ACT_SITE 166 166 BY SIMILARITY.

FT METAL 380 380 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

SQ SEQUENCE 749 AA; 84550 MW; 293854CFB4C826E0 CRC64

Query Match Score 69.2%; Score 36; DB 1; Length 749;

Best Local Similarity 70.0%; Pred. No. 18;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AF04195; AAC64258_1; -

FT EMBL; AF153419; AAG3369_1; -

FT Genew; HGNC; 5959; IKBKAP.

FT MIM; 603722; -

FT MIM; 223900; -

FT GO; GO:0008607; F:phosphorylase kinase, regulator activity; TAS.

FT GO; GO:0004871; F:signal transducer activity; TAS.

FT GO; GO:0006955; P:immune response; TAS.

FT GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

FT InterPro; IPR00649; IKI3.

FT Pfam; PF04762; KI3_1.

KW Phosphorylation; Disease mutation.

FT VARIANT 696 696 R -> P (IN FD; MILD PHENOTYPE; PHOSPHORYLATION IS REDUCED); /FTID=VAR_011327.

FT CONFLICT 304 304 R -> W (IN REF. 2).

FT CONFLICT 312 312 K -> E (IN REF. 2).

FT CONFLICT 754 754 P -> L (IN REF. 2).

FT CONFLICT 961 961 C -> G (IN REF. 3).

FT CONFLICT 1072 1072 S -> C (IN REF. 1).

FT CONFLICT 1158 1158 P -> L (IN REF. 3).

FT CONFLICT 1320 1320 I -> V (IN REF. 3).

SQ SEQUENCE 1332 AA: 150191 MW: 3FD65FAB554D923 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 1332;

Best Local Similarity 60.0%; Pred. No. 78;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 MRQAFYEFD 10

Db . 1240 LKVLFLEFFD 1249

RESULT 4

ID PHOR_ECOLI STANDARD; PRT; 431 AA.

AC P08400;

DT 01-AUG-1988 (Rel. 08; Created)

DT 01-AUG-1988 (Rel. 08; Last sequence update)

DT 28-FEB-2003 (Rel. 41; Last annotation update)

DE Phosphate regulon sensor protein phor (EC 2.7.3.-).

GN PHOR OR NMPB OR B0400.

OS Escherichia coli.

CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

OX NCBI_TAXID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=87169739; PubMed=3550103;

RA Makino K.; Shinagawa H.; Amemura M.; Nakata A.;

RT "Nucleotide sequence of the phor gene, a regulatory gene for the phosphate regulon of Escherichia coli.";

J. Mol. Biol. 192:549-556(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

RA Federspiel N.; Hyman R.; Kalman S.; Komp C.; Kurdi O.; Lew H.; Lin D.; Namath A.; Oefner P.; Roberts D.; Schramm S.; Davis R.W.; Submitted (NOV 1996) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SUBCELLULAR LOCATION

RX MEDLINE=90251245; PubMed=2187152;

RA Yamada M.; Makino K.; Shinagawa H.; Nakata A.;

RT "Regulation of the phosphate regulon of Escherichia coli: properties of phor deletion mutants and subcellular localization of phor protein.";

RL Mol. Gen. Genet. 220:366-372(1990).

RN [5]

RP TOPOLOGY.

RX MEDLINE=933102503; PubMed=8391104;

RA Scholten M.; Tomassen J.;

RT "Topology of the phor protein of Escherichia coli and functional analysis of internal deletion mutants.";

RL Mol. Microbiol. 8:269-275(1993).

-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PHOR/PHOB INVOLVED IN THE PHOSPHATE REGULON GENES EXPRESSION. PHOR MAY FUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT ANALYSIS OF INTERNAL DELETION MUTANTS.

CC -!- PHOSPHORYLATES PHOB IN RESPONSE TO ENVIRONMENTAL SIGNALS.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

CC -!- SIMILARITY: Contains 1 histidine kinase domain.

CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See, <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -!- EMBL: X04704; CAA28409_1; -

DR EMBL; AE000146; AAC73503_1; -

DR EMBL; U73857; AAB18124_1; -

DR PIR; A25557; RGICFR.

DR HSPP; P02933; LJOY.

DR EcoGene; EG10733; phoR.

DR InterPro; IPR001594; Arpbind_Atpase.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR003661; His_Kinase.

DR InterPro; IPR005467; His_Kinase.

DR InterPro; IPR000014; PAS_Domain.

DR Pfam; PF02518; HATPase_c_1.

DR Pfam; PF00512; HISKA_1.

DR Pfam; PF00989; PAS_1.

DR PRINTS; PRO0344; BCPRLENSOR.

DR SMART; SM00387; HATPase_c_1.

DR SMART; SM00388; HISKA_1.

DR SMART; SM0091; PAS_1.

DR TIGRFAMS; TIGR00229; sensory_box_1.

DR PROSITE; PS50109; HIS_KIN_1.

DR PROSITE; PS50112; PAS_1.

KW Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Phosphate transport; Complete proteome.

KW DOMAIN 1 9 CYTOPLASMIC (PROBABLE).

FT TRANSMEM 10 28 PERITRANSMEM (PROBABLE).

FT DOMAIN 29 32 PROTRAMEM (PROBABLE).

FT DOMAIN 33 51 CYTOPROTRAMEM (PROBABLE).

FT DOMAIN 52 431 CYTOPLASMIC (PROBABLE).

FT DOMAIN 96 172 PAS (PROBABLE).

FT DOMAIN 210 425 HISTIDINE KINASE.

FT MOD_RES 213 213 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

SQ SEQUENCE 431 AA; 49629 MW; 33883582AF4BB883C CRC64;

Query Match 63.5%; Score 33; DB 1; Length 431;

Best Local Similarity 66.7%; Pred. No. 42;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 KQAFVFFF 10

Db	298 KQFTFEID 306	Db	298 KQFTFEID 306
RESULT 5			
PHOR_SHIDY	STANDARD;	PRT;	431 AA.
ID P45609;			
AC			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DE phosphate regulon sensor protein phor (EC 2.7.3.-).			
GN PHOR.			
OS Shigella dysenteriae.			
Bacteria; proteobacteria; Gammaproteobacteria; Enterobacteriales;			
Enterobacteriaceae; Shigellales.			
NCBI_TaxID=622;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=90078103; PubMed=2556368;			
RA Lee T.Y., Makino K., Shinagawa H., Amemura M., Nakata A.;			
RT "Phosphate regulon in members of the family Enterobacteriaceae: comparison of the phoB-phoR operons of Escherichia coli, Shigella dysenteriae, and Klebsiella pneumoniae.";			
RT J. Bacteriol. 171:6539-6539 (1989)			
RL J. Bacteriol. 171:6539 (1989)			
CC FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PHO/R-PHOB INVOLVED IN THE PHOSPHATE REGULON GENES EXPRESSION. PHOR MAY			
CC FUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT PHOSPHORYLATES PHOB IN RESPONSE TO ENVIRONMENTAL SIGNALS.			
CC SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.			
CC SIMILARITY: Contains 1 histidine kinase domain.			
CC SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR EMBL; M31793; AAA26536; 1.			
DR PIR; B44733; B44753.			
DR HSSP; P02933; 1JOY.			
DR InterPro; IPR03594; ATPbind_ATPase.			
DR InterPro; IPR003661; His_kinA.			
DR InterPro; IPR005467; His_Kinase.			
DR InterPro; IPR000014; PAS_domain.			
DR Pfam; PF02518; HATPase_c; 1.			
DR Pfam; PF00512; HISKA; 1.			
DR Pfam; PF00989; PAS; 1.			
DR SMART; SM00387; HATPase_c; 1.			
DR SMART; SM00388; HISKA; 1.			
DR SMART; SM00091; PAS; 1.			
DR PROSITE; TIGR00229; sensory_box; 1.			
DR PROSITE; PS50009; HIS_KIN; 1.			
DR PROSITE; PS50112; PAS; 1.			
KW Sensory transduction; Transferase; Kinase; phosphorylation;			
KW Transmembrane; Inner membrane; Phosphotransport.			
FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).			
FT TRANSMEM 14 34 POTENTIAL.			
FT TRANSMEM 35 38 PERIPLASMIC (POTENTIAL).			
FT TRANSMEM 39 59 POTENTIAL.			
FT DOMAIN 60 431 CYTOPLASMIC (POTENTIAL).			
FT DOMAIN 96 167 PAS.			
FT DOMAIN 210 425 HISTIDINE KINASE.			
FT MOD_RES 213 213 PHOSPHORYLATION (AUTO-). (BY SIMILARITY).			
SQ SEQUENCE 431 AA: 497/02 MW: ODD84 FC268253E0 CRC64;			
Query Match 63 58; Score 33; DB 1; Length 431;			
Best Local Similarity 66 78; Pred No. 42;			
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
SQ SEQUENCE 538 AA: 60851 MW: D7B31D2A15BCD6E1 CRC64;			

Query Match 63.5%; Score 33; DB 1; Length 538;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 QAFVFFED 10
 Db 234 QAILFED 241

RESULT 7
GPH_SNP7 STANDARD; PRT; 212 AA.

AC Q55039; PRT; 212 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoglycolate phosphatase (EC 3.1.3.18) (Pgp).
 GN CBBZ.
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1140; MW: 47AD62037D44D33B CRC64;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9627262; PubMed=0654968;
 RA Liu Y., Tsiorres N.F.;
 RT "An unusual gene arrangement for the putative chromosome replication
 origin and circadian expression of dnaN in Synechococcus sp. strain
 PCC 7942."
 RL Gene 172:105-109(1996);
 CC -!- CATALYTIC ACTIVITY: 2-phosphoglycolate + H(2)O = glycolate +
 phosphate.
 CC -!- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC SEQUENCE FROM N.A.
 RX MEDLINE=9627262; PubMed=0654968;
 RA Liu Y., Tsiorres N.F.;
 RT "An unusual gene arrangement for the putative chromosome replication
 origin and circadian expression of dnaN in Synechococcus sp. strain
 PCC 7942."
 RL Gene 172:105-109(1996);
 CC -!- CATALYTIC ACTIVITY: 2-phosphoglycolate + H(2)O = glycolate +
 phosphate.
 CC -!- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC SEQUENCE FROM N.A.
 RX MEDLINE=9627262; PubMed=0654968;
 RA Liu Y., Tsiorres N.F.;
 RT "An unusual gene arrangement for the putative chromosome replication
 origin and circadian expression of dnaN in Synechococcus sp. strain
 PCC 7942."
 RL Gene 172:105-109(1996);
 CC -!- CATALYTIC ACTIVITY: 2-phosphoglycolate + H(2)O = glycolate +
 phosphate.
 CC -!- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC SEQUENCE FROM N.A.
 RX MEDLINE=9627262; PubMed=0654968;
 RA Liu Y., Tsiorres N.F.;
 RT "An unusual gene arrangement for the putative chromosome replication
 origin and circadian expression of dnaN in Synechococcus sp. strain
 PCC 7942."
 RL Gene 172:105-109(1996);
 CC -!- CATALYTIC ACTIVITY: 2-phosphoglycolate + H(2)O = glycolate +
 phosphate.
 CC -!- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.

Query Match 61.5%; Score 32; DB 1; Length 395;
 Best Local Similarity 60.0%; Pred. No. 61;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

Oy 3 QAFVFFED 10
 Db 2 QAILFED 9

RESULT 8
Y414_METJA STANDARD; PRT; 395 AA.
 AC Q57857;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Hypothetical protein MJ0414.
 GN Methanococcus jannaschii.
 OS Archaea; Euryarchaeota; Methanococci; Methanococcaceae;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190; MW: 805439166DECECF CRC64;
 RN [1]

Query Match 61.5%; Score 32; DB 1; Length 212;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

Oy 3 QAFVFFED 10
 Db 2 QAILFED 9

RESULT 9
ECSB_BACSU STANDARD; PRT; 408 AA.
 AC P55340;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein csB.
 GN EcsB OR PRSP.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96146051; PubMed=8581172;
 RA Leskela S., Kontinen V.P., Sarvas M.;
 RT "Molecular analysis of an operon in *Bacillus subtilis* encoding a
 novel ABC transporter with a role in exoprotein production,"
 RT Sporulation and competence;"
 RL Microbiology 142:71-77(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98240224; PubMed=9579061;
 RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
 RT Wedler H., Venema G., Bron S.;
 RT "The 172 kb prkA-addA region from 83 degrees to 97 degrees of the
 BC *Bacillus subtilis* chromosome contains several dysfunctional genes,
 RT the glyB marker, many genes encoding transporter proteins, and the

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferreria S., Fleischmann W., Fosher C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howard T.J., Ke M.H., Ibegwu C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitus A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., McBarry C., Morris J., Mostrefi A., Mount S.M., Moy M., Murphy L., Nixon M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sienk-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svistaks R., Teector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of *Drosophila melanogaster*," *Science* 287:2185-2195 (2000) RRL

[3] RN SEQUENCE OF 1-100 FROM N.A.
RP MEDLINE=87060914; PubMed=3097321;
RX DeJaney S. J., Smith D.F., McClelland A., Sunkel C., Glover D.M.;
RA "Sequence conservation around the 5' ends of the larval serum protein
RT 1 genes of *Drosophila melanogaster*";
RT J. Mol. Biol. 189:1-11 (1986).
RL -!- FUNCTION: LARVAL STORAGE PROTEIN (LSP) WHICH MAY SERVE AS A STORE
CC OF AMINO ACIDS FOR SYNTHESIS OF ADULT PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: HETEROHEXAMER, COMPOSED OF THREE SUBUNITS, ALPHA, BETA,
CC AND GAMMA.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: LARVAL HEMOLYMPH.
CC -!- SIMILARITY: TO ARYLPHORINS AND TO ANTHROPOD-HEMOCYANINS.

This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/annos> or send an email to license@isb-sib.ch).

RESULT 13						
QY	1	MKQAFYFE	8			
	1 1 1 1 : 1 1					
Db	34	MKQKELPSE	41			
SYFB_BACSU		STANDARD;	PRT;	804	AA.	
ID	SYFB_BACSU					
AC	AC_17922; P94540;					
DT	01-NOV-1990 (Rel. 16, Created)					
DT	15-JUL-1993 (Rel. 36, Last sequence update)					
DT	28-FEB-2003 (Rel. 41, Last annotation update)					
DE	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)					
DE	(Phenylalanine--tRNA ligase beta chain) (PhERS).					
GN	PHET.					
OS	Bacillus subtilis.					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus..					
OX	NCBI_TaxID=1423;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=168.					
RX	MEDLINE=91175935; PubMed=2127701;					
RA	Brakhaige A., Wozny M., Putzer H.;					
RT	"Structure and nucleotide sequence of the <i>Bacillus subtilis</i> phenylalanyl-tRNA synthetase genes."					
RT	<i>Biochimie</i> 72:725-734 (1990).					
RL	[2]					
RN	ERRATUM.					
RX	MEDLINE=91134765; PubMed=1903307;					
RA	Wipat A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J., Emmerson P.T., Harwood C.R.;					
RT	"The dnaB-DNA (256 degrees 240 degrees) region of the <i>Bacillus subtilis</i> chromosome containing genes responsible for stress responses, the utilization of plant cell walls and primary metabolism."					
RT	<i>Curr Opin Cell Biol</i> 73:127-127 (1991).					
RL	[3]					
RN	SEQUENCE FROM N.A.					
RC	STRAIN=168.					
RX	MEDLINE=97724191; PubMed=8069504;					
RA	Kunst F.-I., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azvedo V., Berrtero M.G., Bessieres P., Bolotin A., Borchart S.C., Borriss R., Boursier L., Brans A., Braun M., Brignell C., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniell H., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson K.D., Errington J., Fabret C., Ferrari E., Foulger D., Ghosh S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Hilbert B., Holsapple S., Hosono S., Itaya M., Joris B., Karamata D., Kasahara Y., Klaerr-Blaakland M., Klei Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapius A., Larioño S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Manvel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nobre D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Parra Parro V., Pohl T.M., Portelle D., Porwollik S., Prescot A., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Roy R., Rieger M., Rivolta C., Rocha E., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Sorokin A., Tacconi E., Takagi T., Takashashi H., Takenaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni F., Toscano V., Uchiyama S., Vandembol M., Vannier F., Vassarotti R., Viani A., Wambutt R., Wedler E., Weitzeneiger H.,					

RA	Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshihikawa H.-F., Zumstein E., Yoshioka H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";	OS Pasteurella multocida. OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.
RT	Nature 390:249-256(1997)	OX NCBI_TaxID=747;
RL	-!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP + CC diphosphate + L-phenylalanyl-tRNA(Phe).	RN [1]
CC	-!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).	RP SEQUENCE FROM N.A.
CC	-!- SUBUNIT: Tetramer of two alpha and two beta chains (By similarity).	RC STRAIN=PM70;
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.	RX MEDLINE=21145866; PubMed=11248100;
CC	-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 1.	RA May B.-J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S.; Kapur V.; RT "Complete genomic sequence of Pasteurella multocida PM70.";
CC	-!- SIMILARITY: Contains 1 tRNA-binding domain.	RL PROC. NATL. ACAD. SCI. U.S.A. 98:3460-3465(2001);
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC !- CATALYTIC ACTIVITY: ATP + N(2)-formyl-L-N(1)-(5'-phospho-D-ribosyl)glycynamide + L-glutamine + H(2)O = ADP + phosphate + 2-(formamido) N(1)-(5'-phospho-D-ribosyl)acercamidine + L-glutamate.
CC	CC !- PATHWAY: De novo purine biosynthesis; fourth step.	CC !- SUBUNIT: Monomer (By similarity).
CC	CC !- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	CC !- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS FAMILY.
CC	CC !- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.	CC !- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC !- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS FAMILY.
CC	CC DR EMBL; AE006149; AAK03169.1; -.	CC DR EMBL; AE006149; AAK03169.1; -.
DR	DR HAMAP; MF_00283; 1.	DR HAMAP; MF_00419; -; 1.
DR	DR InterPro; IPR005146; B3_4.	DR InterPro; IPR000728; AIRS_related.
DR	DR InterPro; IPR005147; B5.	DR PF00586; AIRS_1.
DR	DR InterPro; IPR005121; Fdx-AntiCB.	DR Pfam; PF02769; AIRS_C_2.
DR	DR InterPro; IPR005132; Phet_bact.	KW Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase; Complete proteome.
DR	DR InterPro; IPR005132; tRNA_bind.	KW NE_BIND 307 ATP (POTENTIAL).
DR	DR Pfam; PF03483; B3_4; 1.	FT ACT_SITE 1137 1137 GATASE (BY SIMILARITY).
DR	DR Pfam; PF03484; B5; 1.	SQ SEQUENCE 1297 AA; 143042 MW; 9362706FFFE34CB4 CRC64;
DR	DR Pfam; PF03117; FDX-ACB; 1.	Query Match 61..58.. Score 32; DB 1; Length 1297;
DR	DR Pfam; PF01588; tRNA_bind; 1.	Best Local Similarity 85..78..; Pred. No. 1..9e+02;
DR	DR TIGR00472; phet_bact; 1.	Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DR	DR PROSITE; PS50886; TRBD; 1.	Qy 4 AFYFEFD 10
KW	KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Magnesium; RNA-binding; tRNA-binding; Complete proteome.	DB 111 AFYFEFD 117
KW	KW DOMAIN 40 155 tRNA-BINDING.	RESULT 15
FT	FT METAL 462 462 MAGNESIUM (BY CARBONYL OXYGEN).	ID YG21_YEAST
FT	FT METAL 468 468 MAGNESIUM (VIA CARBONYL OXYGEN)	ID YG21_YEAST STANDARD; PRT; 283 AA.
FT	FT METAL 471 471 (BY SIMILARITY).	AC P51234;
FT	FT METAL 472 472 MAGNESIUM (BY SIMILARITY).	DT 01-OCT-1996 (Rel. 34, Created)
FT	FT CONFLICT 110 111 KL->NV (IN REF 1).	DT 01-OCT-1996 (Rel. 34, Last sequence update)
FT	FT SEQUENCE 804 AA; 87945 MW; D2337DEAE639E651 CRC64;	DT 01-OCT-1996 (Rel. 34, Last annotation update)
Query Match 61..58.. Score 32; DB 1; Length 804;	DE Hypothetical 32.2 kDa protein in SCM4-MUP1 intergenic region.	
Best Local Similarity 50..08..; Pred. No. 1..2e+02;	GN YG053C.	
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	OS Saccharomyces cerevisiae (Baker's yeast).	
Qy 1 MKGAFVFEED 10	OC Eukaryota; Fungi; Ascomycota; Saccharomycetidae; Saccharomyces.	
Db 683 IKETYVFELD 692	OX NCBL_TaxID=4932;	
RESULT 14	RN [1]	
POR4_PASMU STANDARD; PRT; 1297 AA.	RP SEQUENCE FROM N.A.	
ID POR4_PASMU STANDARD; PRT; 1297 AA.	RA Entian K.D., Rose M., Koetter P., Roehmer A., Sehrsam I., Hempel S.; Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.	
AC Q9CLW4;	RA	
AC 16-OCT-2001 (Rel. 40, Created)	RL	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	CC	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	CC	
DE Phosphotriester-formylglycinamide synthase (EC 6.3.5.3) (FGAM synthase) (FGAMS) (Formylglycinamide ribotide amidotransferase) (FGART) (Formylglycinamide ribotide synthetase).	CC	
DE DE PURL OR PM1085.	CC	
DE DE This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial	CC	

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch).

CC

DR Z72838; CAA97033_1; -

DR PIR; S64347; S64347.

DR SGD; S0003285; YGR052C.

KW Hypothetical protein.

SQ SEQUENCE 283 AA; 32200 MW; 750BF7929396C590 CRC64;

Query Match 59.6%; Score 31; DB 1; Length 283;

Best Local Similarity 50.0%; Pred. No. 69;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKQAFVPEFD 10

:! 1:111:

Db 243 IKGTF1FEFN 252

Search completed: July 24, 2003, 20:06:32
Job time: 4.75325 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 20:01:59 : Search time 7.5974 Seconds

(without alignments)
339.659 Million cell updates/sec

Title: US-09-546-136-1

Perfect score: 52

Sequence: 1 MKQAFVFFED 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTRIMBL_23: *
 - 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rabbit:*
 - 12: sp_rabbit:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriophage:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	49	94.2	144	2	052975	052975 clostridium	
2	41	78.8	452	10	091f173	091f173 arabiopsis	
3	37	71.2	142	2	050600	050600 clostridium	
4	36	69.2	962	12	Q9DUD3	Q9DUD3 pelargonium	
5	35	67.3	761	10	094J14	094J14 oryza sativum	
6	35	67.3	1754	5	Q8I2Q1	Q8I2Q1 plasmidium	
7	34	65.4	285	17	Q9YVC7	Q9YVC7 sulfolobus	
8	34	65.4	374	2	Q9FB53	Q9FB53 thermus fil	
9	34	65.4	1332	4	Q8N516	Q8N516 homo sapien	
10	34	65.4	1333	6	Q8WNKD5	Q8WNKD5 oryctolagus	
11	33	63.5	71	12	Q91FQ1	Q91FQ1 chilio iride	
12	33	63.5	420	10	Q93YQ1	Q93YQ1 arabidopsis	
13	33	63.5	431	16	Q8X99	Q8X99 escherichia	
14	33	63.5	431	16	Q8FkD0	Q8FkD0 escherichia	
15	33	63.5	436	2	Q9RHV5	Q9RHV5 streptococc	
16	33	63.5	436	16	Q8DS90	Q8DS90 streptococc	

Q916a1	pasteurella	17	63.5	53.6	2	Q9L6A1
Q9cnq0	pasteurella	18	63.5	53.6	16	Q9CNO0
Q9Lq7	oryza sativ	19	63.5	55.6	10	Q9LG7
Q9vf45	drosophila	20	63.5	62.7	5	Q9VF45
Q941e6	oryza sativ	21	63.5	69.1	10	Q941E6
Q9ffn4	arabiopsis	22	63.5	71.8	10	Q9FFN4
Q9scv6	arabiopsis	23	63.5	71.8	10	Q9SCV6
Q8gry8	oryza sativ	24	63.5	78.2	10	Q8GRY8
Q8ev5	mycoplasma	25	63.5	82.9	16	Q8EVK5
Q8w5f9	oryza sativ	26	63.5	83.1	10	Q8W5F9
Q9xe23	oryza sativ	27	63.5	95.5	10	Q9XE23
Q9fwk9	oryza sativ	28	63.5	11.04	10	Q9FWK9
Q8ry12	oryza sativ	29	63.5	11.10	10	Q8RYT2
Q9ida3	oryza sativ	30	63.5	12.81	10	Q9IDA3
Q8s211	oryza sativ	31	63.5	13.53	10	Q8S211
Q8ln97	oryza sativ	32	63.5	15.16	10	Q8LN97
Q8sv56	oryza sativ	33	63.5	15.57	10	Q8SV56
Q8lw53	oryza sativ	34	63.5	15.91	10	Q9LDW9
Q91d9	oryza sativ	35	63.5	15.92	10	Q8LQ12
Q8w5n7	oryza sativ	36	63.5	15.97	10	Q8W5M7
Q8h904	oryza sativ	37	63.5	15.97	10	Q8H904
Q8w062	oryza sativ	38	63.5	16.04	10	Q8W062
Q8lr53	oryza sativ	39	63.5	16.05	10	Q8LR53
Q9fw81	oryza sativ	40	63.5	16.26	10	Q9FWB1
Q94db7	oryza sativ	41	63.5	16.26	10	Q94DB7
Q9ayg3	oryza sativ	42	63.5	16.41	10	Q9AYG3
Q8sb37	oryza sativ	43	63.5	16.56	10	Q8SB37
Q8h219	oryza sativ	44	63.5	16.62	10	Q8H219
Q8h525	oryza sativ	45	63.5	17.27	10	Q8H525

ALIGNMENTS

RESULT 1	052975	PRELIMINARY;	PRT;	144 AA.
	ID	052975;		
	AC	052975;		
	DT	01-JUN-1998 (TREMBLrel. 06, Created)		
	DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
	DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)		
	DE	ORF-X1.		
	DR	E and Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types.		
	DR	RT		
	DR	E and Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types.		
	DR	RT		
	DR	DR EMBL: D8841B; BAA24880.1; DR FEMS Microbiol. Lett. 158:215-221(1998).		
	SQ	SEQUENCE 144 AA: 16767 MW; 3AAF7DB7F67670BC CRC64;		
	QY	1 MKAQAFVFFED 10		
	DB	3 LKAQAFVFFED 12		

SEQUENCE FROM N.A.
STRAIN=type E Iwanai;
RX MEDLINE=98126542; PubMed=9465394;
RA Kubota T., Yonekura N., Hariya Y., Isogai E., Amano K.,
RA Fuji N.;
RT "Gene arrangement in the upstream region of Clostridium botulinum type E and Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types.";
RT from that of other types.;
RL FEMS Microbiol. Lett. 158:215-221(1998).
DR EMBL: D8841B; BAA24880.1; DR FEMS Microbiol. Lett. 158:215-221(1998).
SQ SEQUENCE 144 AA: 16767 MW;

Result No.	Score	Query	Match	Length	DB	ID	Description
1	49	94.2	144	2	052975	052975 clostridium	
2	41	78.8	452	10	091f173	091f173 arabiopsis	
3	37	71.2	142	2	050600	050600 clostridium	
4	36	69.2	962	12	Q9DUD3	Q9DUD3 pelargonium	
5	35	67.3	761	10	094J14	094J14 oryza sativum	
6	35	67.3	1754	5	Q8I2Q1	Q8I2Q1 plasmidium	
7	34	65.4	285	17	Q9YVC7	Q9YVC7 sulfolobus	
8	34	65.4	374	2	Q9FB53	Q9FB53 thermus fil	
9	34	65.4	1332	4	Q8N516	Q8N516 homo sapien	
10	34	65.4	1333	6	Q8WNKD5	Q8WNKD5 oryctolagus	
11	33	63.5	71	12	Q91FQ1	Q91FQ1 chilio iride	
12	33	63.5	420	10	Q93YQ1	Q93YQ1 arabidopsis	
13	33	63.5	431	16	Q8X99	Q8X99 escherichia	
14	33	63.5	431	16	Q8FkD0	Q8FkD0 escherichia	
15	33	63.5	436	2	Q9RHV5	Q9RHV5 streptococc	
16	33	63.5	436	16	Q8DS90	Q8DS90 streptococc	

RESULT 2

ID	Q9L173	PRELIMINARY;	PRT;	452 AA.
AC	Q9L173;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			

Best Local Similarity Matches	87.5%; 7;	Pred. No. Mismatches	1.1e+02; 0;	Indels	0;	Gaps	0;		RA
Oy	2 KOAFVFEDF 9								RA Thi-Ngoc H. P., Redder P., Schenk M. E., Therriault C., Tolstrup N.,
Db	563 KQALVFEDF 570								RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
									RA Garrett R.A., Ragan M.A., Sensem C.W., Van der Oost J.
									RT "The complete genome of the Crenarchaeon Sulfolobus solfataricus P2.;"
									RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
									EMBL AE006864; AAK42817; 1.
									DR InterPro IPR005511; SMP-30.
									DR Pfam PF03758; SMP-30; 1.
									KW Complete proteome.
									SQ SEQUENCE 285 AA; 32194 MW; 3FA045545790DA5B CRC64;
RESULT 6									
ID Q8I2Q1	PRELIMINARY;								
AC Q8I2Q1;									
DT 01-MAR-2003 (TRMBLrel. 23, Created)									Query Match Score 34; DB 17; Length 285;
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)									Best Local Similarity 50.0%; Pred. No. 66;
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)									Mismatches 4; Indels 0; Gaps 0;
DE Hypothetical protein.									
GN Plasmodium falciparum (isslate 3D7).									
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.									
OX NCBI_TaxID=36329;									
RN [1]									
RP	SEQUENCE FROM N.A.								
	MEDLINE=22255708;								
	PUBMED=12368867;								
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,									Q9F8S3 ID PRELIMINARY; PRT; 374 AA.
RA Mungall K., Bowman S., Atkin R., Barron A., Brooks K.,									AC Q9F8S3;
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,									DT 01-MAR-2001 (TRMBLrel. 16, Created)
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,									DT 01-MAR-2001 (TRMBLrel. 16, Last sequence update)
RA Cronin A., Davies P., Davies P., Dear P., Dearden F., Doggett J.,									DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,									DE TfII restriction endonuclease.
RA Harper D., Hauser H., Hornsby T., Hollroyd S., Horrocks P.,									GN TfIIR.
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhorou A.,									OS Thermus filiformis.
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,									OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
RA Line A., Maddison M., McLean J.J., McLean J.J., Mooney P., Moule S., Murphy L.,									OC Thermus.
RA Oliver K., Ormond D., Price C., Qualia M.A., Rabnowitsch E.,									OX NCBI_TaxID=276;
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,									RN [1]
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,									RP SEQUENCE FROM N.A.
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,									RA Xu S.-Y., Hsieh P.-C.;
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.,									RT Method for cloning and producing the TfII restriction endonuclease in
FT *Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.;"									RT E. coli; DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL AL929358; CAD51939.1;									DR EMBL AF239324; AAC33969.1;
KW Hypothetical protein.									DR InterPro IPR00294; D12R6_mtRNAse.
SO SEQUENCE 1754 AA; 208589 MW; CB074AEAC63D99DE CRC64;									DR InterPro IPR00252; N6_Mtase.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
									DR EMBL AF239324; AAC33969.1;
									DR InterPro IPR00294; D12R6_mtRNAse.
									DR PR02086; MethylltransfD12; 1.
									DR PR00505; D12R6MtTASE.
									DR PROSITE PS00092; N6_MTASE; 1.
									KW Endonuclease.
									DR Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
			</td						

DR	PROSITE; PS50112; PAS; 1.		DR	InterPro; IPR002917; MMR_HSR1.
KW	Complete proteome.		DR	InterPro; IPR005225; Small_GTP.
SQ	SEQUENCE 431 AA; 49677 MW; 85CBBFA36D72E25 CRC64;		DR	Pfam; PF01926; MMR_HSR1; 1.
Query Match	63.5% Score 33; DB 16; Length 431;		DR	PRINTS; PR00326; GTI1OBG.
Best Local Similarity	66.7%; Pred. No. 1.6e+02;		DR	TIGRFAMS; TIGR00650; MG412; 2.
Matches 6; Conservative 0; Mismatches 3; Indels 0;	Gaps 0;		DR	TIGRFAMS; TIGR00231; small_GTP;
Qy	2 KQAFVFFFD 10		SQ	SEQUENCE 436 AA; 48601 MW; EC52CC8650DED090 CRC64;
Db	298 KQTFFEID 306		Query Match	63.5%; Score 33; DB 2; Length 436;
			Best Local Similarity	75.0%; Pred. No. 1.6e+02;
			Matches 6; Conservative 0; Mismatches 0; Indels 0;	Gaps 0;
RESULT 14			Qy	1 MKQAFVFE 8
Q8FKD0	ID PRELIMINARY; PRT; 431 AA.		Db	:11111 :11111
AC	Q8FKD0;			417 IROAFVFE 424
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Phosphate regulon sensor protein phor (EC 2.7.3.-).			
GN	PHOR OR C0509			
OS	Escherichia coli O6.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=217992;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=06_H1 / CFT073 / ATCC 700928;			
RX	MEDLINE=22388224; PubMedID=12471157;			
RA	Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,			
RA	Rasko D., Buckles E.L., Boutin A., Hackett J.J., Stroud D.,			
RA	Maynew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,			
RA	Mobley H.L.T., Donnenberg M.S., Brattner F.R.,			
RT	"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli".			
RL	PROC. NATL. ACAD. SCI. U.S.A. 99:17020-17024 (2002).			
DR	EMBL; AE016756; AACN8987.1; -			
KW	Transferase; Complete proteome.			
SQ	SEQUENCE 431 AA; 49630 MW; 3EE092456D432FFE CRC64;			
Query Match	63.5% Score 33; DB 16; Length 431;			
Best Local Similarity	66.7%; Pred. No. 1.6e+02;			
Matches 6; Conservative 0; Mismatches 3; Indels 0;	Gaps 0;			
Qy	2 KQAFVFFFD 10			
Db	298 KQTFFEID 306			
RESULT 15				
Q9RHV5	ID Q9RHV5 PRELIMINARY; PRT; 436 AA.			
AC	Q9RHV5;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Phosphoglycerate dehydrogenase.			
GN	PGDA.			
OS	Streptococcus mutans.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1309;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=M78148;			
RA	Kawabata S., Terao Y., Hamada S.;			
RT	"Molecular cloning, sequence and characterization of a novel streptococcal phosphoglycerate dehydrogenase gene.";			
RT	Oral Microbiol. Immunol. 15:58-62 (2001).			
RL	EMBL; AB016077; BA888B3.1; -			
DR	InterPro; IPR005289; GTP-binding_dom.			
DR	InterPro; IPR006073; GTP1_OBG.			

Result No.	Score	Query	Match Length	Length DB	ID	Description
1	98	13.6	274	23	ABP7384	Candida albicans e
2	96.5	13.3	1224	21	AAB18258	Plasmodium falciparum
3	95	13.1	236	22	AAB61576	Murine prolactin-1
4	90.5	12.5	297	19	AAC59151	S. gordoni rgg1 p
5	90.5	12.5	453	22	AAC69944	EPA binding domain
6	90.5	12.5	572	23	ABB09495	AuNPV poly(A) poly
7	90.5	12.5	1847	23	ABP73701	Candida albicans e
8	89.5	12.4	1847	21	AAV85277	C. albicans CAJL03
9	88.5	12.2	1247	21	ABB18215	Plasmodium falciparum

XX The present invention relates to ERA binding domain polypeptides
 CC (AAGS9559-AAGC9989 and AM00010-AM00021). The era gene in Escherichia
 CC coli codes for an essential GTPase protein able to autophosphorylate at
 CC serine and/or threonine residues. The protein has potential antimicrobial
 CC and antibacterial activity and is useful in screening for antagonists,
 CC agonists and for compounds with antibiotic activity. The proteins are
 CC also useful in determining their role in pathogenesis of infection,
 CC dysfunction and disease and could be used as part of a vaccine and/or
 CC peptide therapy.

XX Sequence 453 AA;

Query Match 12.5%; Score 90.5; DB 22; Length 453;
 Best Local Similarity 27.6%; Pred. No. 0.85; Mismatches 23; Indels 31; Gaps 7;
 Matches 43; Conservative 43; Mismatches 59; Indels 31; Gaps 7;
 Qy 13 ENLSSGGSYHLEVKQNCSPNVDKTFIDGLYIK-----NSGVILD-----KVD 61
 Db 174 EKISQEHSKEKNSVIAKIGPKVSKTINSLLKKPMTSKAGTLDTVLPIKVN 233
 Qy 62 LKNVISLVALKRDLYLSSLSSNNK---QIKKFKNKHNKHLNKNFNYVINEDIEKRTKNGI 119
 Db 234 YKNYIFI----DTAGMSKKSKTKNIEKFCKIQLQTIEKSHLTLIIIDAKDQISKQDL 288
 Qy 120 LEE-----VILNKA-LISL-LGNNEENLQ 142
 Db 289 LLSSFIEKSGRPLIVINKCDLSSLKREKKNLNLK 324

RESULT 6
 ABB09495 ID ABB09495 standard; Protein: 572 AA.

AC ABB09495; FT 01-JUL-2002 (first entry)

DE AmEPV poly(A) polymerase large subunit (AMV038) amino acid sequence.
 KW AmEPV; gene therapy; viral vector; chromosome mapping; gene mapping;
 KW genetic deficiency disorder; polymerase.

XX Amstacta moorei entomopoxvirus.

XX Key Location/Qualifiers

FT Misc-difference 530 .531
 FT /note= "encoded by ATAAAGGC"

PN WO200212526-A2.

XX PD 14-FEB-2002.

XX PF 10-AUG-2001; 2001WO-US25287.

XX PR 10-AUG-2000; 2000US-224479P.

XX PR 14-SEP-2000; 2000US-0662254.

XX PA (UYFL) UNIV FLORIDA.

XX PI Moyer RW, Li Y, Bawden AL;

XX DR WPI: 2002-227161/28.

XX DR N-PSDB; ABL55642.

XX Novel recombinant entomopox virus vector useful for delivering
 PT PT Polynucleotide encoding protein to vertebrate cell, comprises
 PT PT Polynucleotide encoding protein operably linked with heterologous
 PT promoter sequence -

XX Claim 73; Page 123-124; 326pp; English.

XX The invention relates to a recombinant entomopox virus (EPV) vector,

CC comprising a polynucleotide encoding a protein operably linked with a
 CC heterologous promoter sequence. The invention also concerns methods for
 CC providing gene therapy for genetic deficiency disorders. Vectors of the
 CC invention are useful for delivering Polynucleotide encoding a protein
 CC to a vertebrate cell preferably a mammalian cell, such as a human cell.
 CC The vector is introduced into the vertebrate cell by infection in a viral
 CC particle, or by transfection, transduction, or injection either in vitro
 CC or in vivo. The vector is useful for the delivery and expression of
 CC biologically useful proteins in gene therapy protocols, and for
 CC delivering large DNA segments for engineering of vertebrate cells.
 CC Polynucleotides of the invention have applications in techniques such as
 CC their use as insertion sites for foreign genes of interest, hybridisation
 CC probes for chromosome and gene mapping, in PCR technologies, and in the
 CC production of sense or antisense nucleic acids. Vectors of the invention
 CC provide for stable integration and expression of heterologous DNA in host
 CC cells, and are adapted for accepting large heterologous polynucleotide
 CC inserts which can be delivered in an infected or transformed cell and
 CC expressed in a stable fraction. The current sequence represents the
 CC amstacta moorei entomopoxvirus (AmEPV) poly(A) polymerase large subunit
 CC (AMV038) amino acid sequence.

SQ Sequence 572 AA;
 Query Match 12.5%; Score 90.5; DB 23; Length 572;
 Best Local Similarity 24.0%; Pred. No. 1.2;
 Matches 36; Conservative 25; Mismatches 52; Indels 37; Gaps 6;
 SQ Sequence 572 AA;

	Query Match	Best Local Similarity	Score	Length
Matches	36;	Conservative	24.0%	572;
Db	227	HLTIGHDTC-----LSFISPFITGHISLYKXKNIIFDCIFLDNSSTINVANSKLNNIYFI	281	76
Qy	22	IHLERKVKONCSPNYPDYFKTFIDGYLYIKNKGYILD-----KYDLKVNISLVALKRDL-	114	76
Db	227	IHLTIGHDTC-----LSFISPFITGHISLYKXKNIIFDCIFLDNSSTINVANSKLNNIYFI	281	281
Qy	77	-SLSLSNN-----KQIKKFKNKHNHL--KRNFKNLVINEDEIEKRI	114	114
Db	282	DPGQMLNFRMFLSENRFSYKYEKMEESLNKYKTLNLYFVNNNNKFNKORLNWLKSVD	341	341
Qy	115	TKNGLEEVLNKMLSLILGNEENLQIS	144	144
Db	342	CRNNEPYTIVNTLISI-----RELIDS	366	366

RESULT 7
 ABP73701
 ID ABP73701 standard; Protein: 1847 AA.
 XX
 AC ABP73701;
 DT 30-JAN-2003 (first entry)
 DE Candida albicans essential protein SEQ ID NO 7538.
 XX
 KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; Candida albicans; fungicide; antifungal.
 DE Candida albicans.
 XX
 PN WO200253728-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001WO-US49486.
 XX
 PR 29-DEC-2000; 2000US-259128P.
 PR 20-FEB-2001; 2001US-0793024.
 PR 22-AUG-2001; 2001US-314050P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 DR N-PSDB; ABZ32251.
 XX

PT Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele
 PT of a gene and placing other allele of the gene under conditional
 PT expression -

XX Claim 44; SEQ ID NO 7538; 167pp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthetic, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of C. albicans cells and for
 CC treating infection by C. albicans. The present sequence is that of an
 CC essential Candida albicans protein used in the method of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.

XX Sequence 1847 AA;

Query Match 12.5%; Score 90.5%; DB 23; Length 1847;
 Best Local Similarity 23.3%; Pred. No. 5.7; Mismatches 25; Indels 53; Gaps 7;

Matches 40; Conservative 54; Mismatches 54; Indels 53; Gaps 7;

CC Sequence 1847 AA;

CC Query Match 12.4%; Score 89.5%; DB 21; Length 1847;

CC Best Local Similarity 23.3%; Pred. No. 7.2; Mismatches 26; Indels 53; Gaps 7;

CC Matches 40; Conservative 54; Mismatches 54; Indels 53; Gaps 7;

CC Query 19 SGSIHLEVKVQ-----NCSPIHYDFYK1-----TFID-----GYL 47

CC Db 1249 SSSITLNQLRVEELEFEKLINCPQLDLNFTWCGNOFGDLQIDASNVFDNQASTQAFF 1308

CC Qy 48 YIKNKSGVILDKYDLKVNISLVALKRDYLSSLNSNNKQ-----IKKFKNIKNHKLKN- 99

CC Db 1309 SFINQRNLQIYLSEFSVSKRTREYYSKVLTNDKEFVNRTPKVLTFLNLYSFKNF 1368

CC Qy 100 -----KFNLYVINEDIEKRITKNGILLEVLNLKMLLSILGNEENIL 141

CC Db 1369 EVQKYEWLDQKFNMSSLLAEEVNAQ--KNGTLDFSVLTKVPR--LLCQTSNL 1416

CC {

CC RESULT 8

AY85277 04-JUL-2000 (first entry)

XX DE AAB18215 standard; Protein: 1247 AA.

XX ID AAB18215 standard; Protein: 1247 AA.

XX XX AAB18215;

XX AC AAB18215;

XX DT 07-NOV-2000 (first entry)

XX DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:72.

XX XX AAB18215;

XX KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;

XX KW antimalarial; malaria; protozoa; infection; insecticide.

XX PD 23-MAR-2000.

XX XX OS Plasmodium falciparum.

XX XX

PF 13-SEP-1999; 99WO-EP07376.

XX	PR 11-SEP-1998; 98EP-0402255.
XX	PA (HMRI) HOECHST MARION ROUSSEL.
XX	PI Lalanne J, Rocher C, Chalwatzis N, Leeuw T, Margerie D, Nitsche A;
XX	PI Reinhard Rupp J;
XX	DR 2000-271469/23.
XX	DR N-PSDB; AAA10735.
XX	Novel genes from <i>Candida albicans</i> , useful for screening for antifungal drugs for treatment or prevention of fungal infection - Disclosure; Page 93-100; 139pp; English.
XX	This sequence represents the protein encoded by the <i>Candida albicans</i> Cau039 gene. The invention relates to eight nucleotide sequences representing essential <i>C. albicans</i> genes, and the polypeptides, and a method for they encode. An antibody against the polypeptides, and a method for screening for antimycotic substances using one of the essential genes or the peptides encoded by them as a target is also included in the invention. The method may be used to screen for substances that inhibit the expression of the target essential <i>Candida albicans</i> or <i>Aspergillus</i> fumigatus genes or inhibit the activity of essential proteins from these species. This method is particularly useful for screening for inhibitors of 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK) and/or dihydropteroate synthase (DHPS). The method may also be used to identify antimycete substances acting on other mycete species. These inhibitors may be used to treat infections caused by these organisms or may be used prophylactically to prevent infection in immunosuppressed individuals. The nucleotide sequences may be used to identify functionally similar genes in other mycete species, and may also be used as a probe to screen a. <i>C. albicans</i> genomic library. The genes and polypeptides may also be used to identify fungal infections. The new method of screening for antimycotic substances using essential genes or proteins allows the identification of drugs which will only inhibit growth of specific mycete species.
XX	Sequence 1847 AA;
XX	Query Match 12.5%; Score 90.5%; DB 23; Length 1847;
XX	Best Local Similarity 23.3%; Pred. No. 5.7; Mismatches 25; Indels 53; Gaps 7;
XX	Matches 40; Conservative 54; Mismatches 54; Indels 53; Gaps 7;
XX	CC Sequence 1847 AA;
XX	CC Query Match 12.4%; Score 89.5%; DB 21; Length 1847;
XX	CC Best Local Similarity 23.3%; Pred. No. 7.2; Mismatches 26; Indels 53; Gaps 7;
XX	CC Matches 40; Conservative 54; Mismatches 54; Indels 53; Gaps 7;
XX	CC Query 19 SGSIHLEVKVQ-----NCSPIHYDFYK1-----TFID-----GYL 47
XX	CC Db 1249 SSSITLNQLRVEELEFEKLINCPQLDLNFTWCGNOFGDLQIDASNVFDNQASTQAFF 1308
XX	CC Qy 48 YIKNKSGVILDKYDLKVNISLVALKRDYLSSLNSNNKQ-----IKKFKNIKNHKLKN- 99
XX	CC Db 1309 SFINQRNLQIYLSEFSVSKRTREYYSKVLTNDKEFVNRTPKVLTFLNLYSFKNF 1368
XX	CC Qy 100 -----KFNLYVINEDIEKRITKNGILLEVLNLKMLLSILGNEENIL 141
XX	CC Db 1369 EVQKYEWLDQKFNMSSLLAEEVNAQ--KNGTLDFSVLTKVPR--LLCQTSNL 1416
XX	CC {
XX	CC RESULT 9
XX	AAB18215
XX	ID AAB18215 standard; Protein: 1247 AA.
XX	XX AAB18215;
XX	AC AAB18215;
XX	DT 07-NOV-2000 (first entry)
XX	DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:72.
XX	XX AAB18215;
XX	KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
XX	KW antimalarial; malaria; protozoa; infection; insecticide.
XX	PD 23-MAR-2000.
XX	OS Plasmodium falciparum.
XX	XX

PN WO200025728-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US26796.
 XX
 PR 05-NOV-1998; 98US-0107131.
 XX
 PA (HOFF/) HOFFMAN S.
 PA (CARU/) CARUCCI D.
 PA (GARD/) GARDNER M.
 PA (VENT/) VENTER J. C.
 XX
 PI Hoffman S., Carucci D., Gardner M., Venter J.C.,
 XX
 DR WPI: 2000-365347/31.
 XX
 PT Proteins encoded by chromosome 2 of the human malaria parasite,
 PT Plasmodium falciparum, useful as antimalarial vaccines and in the
 PT diagnosis of P. falciparum infection -
 XX
 PS Disclosure; Page 168-171; 577pp; English.
 XX
 CC The present invention describes proteins and their fragments (I) encoded
 CC by chromosome 2 of the human malaria parasite. Plasmodium falciparum
 CC vaccines against P. falciparum infection comprising (I) or (II).
 CC (I) and (II) are useful for the development of vaccines against
 CC P. falciparum infection (I) and polyclonal antisera or a monoclonal
 CC antibody raised to immunogens comprising the sequences of (I), are
 CC useful in the detection of infection with P. falciparum. Furthermore,
 CC (I) (especially when they are rifins or secreted membrane proteins)
 CC can aid the identification of drugs to treat or prevent P. falciparum
 CC infection, or they can be used to identify drug resistance in
 CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
 CC subsequent identification of proteins encoded by it will help to expand
 CC our understanding of parasite biology, a process hampered by the
 CC complexity of the parasitic lifecycle, and provide new targets for
 CC vaccine and drug development. Parasite resistance to drugs and mosquito
 CC resistance to insecticides have led to a resurgence of malaria in many
 CC parts of the world, and there is a pressing need for vaccines and new
 CC drugs. AAB7028 to AAA7028 and AAB1814 to AAB18352 represent nucleotide
 CC and protein sequences given in the present invention, but which are not
 CC specifically mentioned within the specification.
 XX
 Sequence 1247 AA;
 Query Match 12.28; Score 88.5; DB 21; Length 1247;
 Best Local Similarity 23.18; Pred. No. 5.4;
 Matches 39; Conservative 22; Mismatches 49; Indels 59; Gaps 7;
 QY :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 190 QLDEWHSDRGA-----NKNSRTDTNKLINNNYFRKEIYMKKEESDLLNNENDKKN 241
 QY 65 VISVALKRDYLSSLSNNRQI-----KKPKNIKRNHLKNN-----100
 Db 242 HGDFYNIKSDDL---NNSNIGYQRKRRKKKKFIRKAKRKRKNQGYVEVDHLDNTL 296
 QY 101 FNL-----YVINEDIEKRITKGILFEVLNKLMLSILLGNEENL 140
 Db 297 FNIYEDNIALYNYENFDYKFLYKGLIDN-----SYKGNNNOL 337
 RESULT 10
 AAY54040 standard; Protein; 471 AA.
 XX
 AC AAY54040;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Amino acid sequence of a yeast SceI endonuclease.

XX SceI endonuclease; phosphodiester bond; yeast; genetic engineering;
 KW PCR; polymerase chain reaction; gene cloning.
 XX Saccharomyces cerevisiae.
 OS XX
 PN EP972836-A2.
 XX
 PD 19-JAN-2000.
 XX
 PF 21-MAY-1999; 99EP-0110008.
 XX
 PR 22-MAY-1998; 98JP-0141861.
 XX
 PA (RIKA) INST PHYSICAL & CHEM RES.
 XX
 PI Morishima N., Shibata T., Mizumura H.;
 XX
 DR WPI: 2000-099856/09.
 DR N-PSDB; AA237082.
 XX
 PT New modified endonuclease capable of recognizing specific nucleotide
 sequence, useful for genetic engineering techniques -
 XX
 PS Disclosure; Fig 1; 43pp; English.
 XX
 CC The present sequence represents a yeast SceI endonuclease. The
 CC endonuclease hydrolyses the phosphodiester bond of a polynucleotide
 CC chain. The endonuclease is the 50 kDa subunit of a yeast endonuclease.
 CC The endonuclease gene was modified so that it could be
 CC mass-produced in an expression system such as E. coli or yeast. The
 CC endonuclease polynucleotide sequence was modified by substituting
 CC codons that are unique to mitochondria (the gene is expressed in
 CC mitochondria) with universal codons. The endonuclease cuts molecules
 CC within sequence AA237082, and is therefore useful in genetic engineering
 CC techniques such as PCR (polymerase chain reaction) for cloning,
 CC amplifying and analysing genes.
 XX
 SQ Sequence 471 AA;
 Query Match 12.0%; Score 87; DB 21; Length 471;
 Best Local Similarity 28.6%; Pred. No. 2.1;
 Matches 30; Conservative 18; Mismatches 33; Indels 24; Gaps 4;
 QY 32 SPNDYFKITFIDSYLYIKNKGIVLDKYD-----LKNVISLVALKDYLSSL 78
 Db 86 SKN1IDYKLL-YFYILNKIKEDIINYNNNNNISLYKNEELKNIINNLKLSNIEL 143
 QY 79 SLSNNKQIKFKFNKFNKBLKNNKFENLYVINEDIEKRITKGILLEEV 123
 Db 144 NLSRNFY----LIDKYLINKTYKL--DILNIPNNYFNNI 179
 RESULT 11
 ID AAB18198
 XX
 AC AAB18198;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:55.
 XX
 KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
 KW antimalarial; malaria; protozoacide; infection; insecticide.
 XX
 OS Plasmodium falciparum.
 XX
 PN WO200025728-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US26796.

XX 05-NOV-1998; 98US-0107131.
 XX (HOFF/) HOFFMAN S.
 PA (CAR/) CARUCCI D.
 PA (GARD/) GARDNER M.
 PA (VENT/) VENTER J C.
 PI Hoffman S, Carucci D, Gardner M, Venter JC;
 XX DR WPI; 2000-365347/31.
 XX Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
 XX Disclosure; Page 126-133; 57pp; English.
 XX The present invention describes proteins and their fragments (1) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).
 CC (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AA70078 to AAA70287 and AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.

XX Sequence 2539 AA;

Query Match 12.0%; Score 86.5; DB 21; Length 2539;
 Best Local Similarity 26.7%; Pred. No. 23;
 Matches 36; Conservative 26; Mismatches 36; Indels 37; Gaps 8;

Qy 36 DYFKITIDGYLI---KKNKGIVLID--KYDLKVNIVSLLALKDYSLSLSNNKQIKR 88
 Db 617 NYSSOTISSLLIPSQNKNTKLNYKHSYTKNMN----NDYTNNKYIINKQKNI 671

Qy 89 FKNIKNHKLKNAKFN-LVYINDEIKR-----ITNGILLEEVILRNKMLL---- 130
 Db 672 YNNIKN-NIKKIRYLN-ISHOKEKKKKLTFKKYMKRECLLNSTLNKLIIPHDCRK 730

Qy 131 -SILLG----NEEN 139
 Db 731 GTMILNQHNLNEEN 745

RESULT 12
 ABP7374 DT 30-JAN-2003 (first entry)
 ID ABP73774 Standard; Protein: 1948 AA.
 AC ABP73774;
 XX DT Candida albicans essential protein SEQ ID NO 7611.
 KW Fungus; Yeast; tetracyclin; Promoter: GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; Candida albicans; fungicide; antifungal.

OS Candida albicans.
 XX WO200253728-A2.
 PN XX 11-JUL-2002.
 PD XX 26-DEC-2001; 2001WO-US49486.
 PF XX 29-DEC-2000; 2000US-259128P.
 PR XX 20-FEB-2001; 2001US-079024.
 PR XX 22-AUG-2001; 2001US-314050P.
 PA (ELIT-) ELITRA PHARM INC.
 PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 XX DR WPI; 2002-566634/60.
 DR N-PSDB; ABZ32324.

XX Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression

CC Claim 44; SEQ ID NO 7611; 167pp + Sequence Listing; English.

CC The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the CC promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

CC Sequence 1948 AA;

CC Query Match Score 86; DB 23; Length 1948;
 CC Best Local Similarity 22.3%; Pred. No. 18;
 CC Matches 43; Conservative 27; Mismatches 67; Indels 56; Gaps 5;
 CC 37

Qy 2 ELKQA----FVFEFDENLSSSGSTHLERVKQNCSPNWKY-----
 Db 1750 ELKQAGELDFLKHLNQREDSEALKTTELQNSKMSTSFDIRDQOKLRNELLVKEENFS 1809

Qy 38 -----EKITFIDGYL-----
 Db 1810 LVTKTNKELNRYSDLERKLYSNEQLKXWESKLYKDTLSKALODALNEHEADTKVQRSI 1869

Qy 74 DYLSLSLSNKNOIKKEFKNKNKFKNLY----VINEDEKRTKNGILEEVILNK 127
 Db 1870 KOLEIRIVEONESOLSKRYNDENFYQNKINHYKSSTDIIHNENKEQLQKSIQRENI-E 1927

Qy 128 MLLSILIGNEEML 140
 Db 1928 MKESMLMLQKEVL 1940

RESULT 13		Drosophila melanogaster polypeptide SEQ ID NO 8211.
AAW48742	XX	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
ID AAW48742 standard; Protein: 469 AA.	XX	KW KW
XX	AC	Drosophila melanogaster.
XX	AC AAW48742;	OS OS
DT 01-OCT-1998 (first entry)	PN WO200171042-A2.	XX PN
XX	PD 27-SEP-2001.	XX PD
DE Human granulocytic ehrlichiosis isolate NCH-1 E7 protéin.	PF 23-MAR-2001; 2001WO-US09231.	XX PF
XX	KW Human; granulocytic ehrlichiosis; HGE; aOHGE; diagnosis; vaccine; detection; infection.	XX PR 23-MAR-2000; 2000US-19137P.
XX	XX OS Homo sapiens.	PR 11-JUL-2000; 2000US-0614150.
XX	PN WO9814584 A2.	PA (PEKE) PE CORP NY.
XX	PD 09-APR-1998.	XX PT Venter JC, Adams M, Li PWD, Myers EW;
XX	PF 30-SEP-1997; 97WO-US17675.	XX DR WPI: 2001-656860/75.
XX	DR N-PSDB; ABL04576.	XX DR N-PSDB; ABL04576.
PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	XX PT	XX PT
CC Disclosure; SEQ ID NO 8211; 21pp + Sequence Listing; English.	XX PS	XX PS
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1617-ABL16176; ABL1617-ABL16175), expressed DNA sequences (ABB57737-ABB72072).	XX CC	XX CC
CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	XX SQ Sequence 481 AA;	CC CC
CC	Query Match 11.8%; Score 85.5; DB 22; Length 481;	CC CC
CC Best Local Similarity 24.6%; Pred. No. 3;	Best Local Similarity 24.6%;	CC CC
CC Matches 33; Conservative 29; Mismatches 45; Indels 27; Gaps 6;	Matches 33; Conservative 29; Mismatches 45; Indels 27; Gaps 6;	CC CC
Db 8 VFEFDENLSSSGSSTHLEVKQNCSPNYD--YFKITFIDGYLYIKNSGVIL--DKYD 61	Oy 8 VFEFDENLSSSGSSTHLEVKQNCSPNYD--YFKITFIDGYLYIKNSGVIL--DKYD 61	Db 8 VSEDELQTSNNGIGDCDVHQSDKLDSDPFCQILLINLYLSNVQGEVSVASEPD 67
Db 62 L---KVNISVALKRDSLSSLNNQKIKKFKNKKHKLKNNFLNYINEDIKRITKN 117	Qy 62 L---KVNISVALKRDSLSSLNNQKIKKFKNKKHKLKNNFLNYINEDIKRITKN 117	Db 68 FAISESQSLKLKETHV---NN--LQSYTKVKKHL-----QKIRRLKKD 110
Db 118 GILEEVILNKML 131	Qy 118 GILEEVILNKML 131	Db 111 LGLEQIAVSQMLLT 124
Db 111 LGLEQIAVSQMLLT 124		
RESULT 15		
AAV95065	ID AAV95065 standard; Protein: 707 AA.	XX AC AAV95065;
XX	AC	XX DT 23-JUN-2000 (first entry)
RESULT 14		
ABB60473	ID ABB60473 standard; Protein: 481 AA.	XX AC ABB60473;
XX	AC	XX DE
XX	XX	XX KW
XX	XX	XX KW
XX	XX	XX KW
DT 26-MAR-2002 (first entry)		

OS Candida albicans.
 XX EP962401-A2.
 PN XX
 PD 01-MAR-2000.
 XX PF 23-DEC-1998; 98EP-0310694.
 XX PR 14-AUG-1998; 98GB-0017796.
 XX PA (JAN) JANSSEN PHARM NV.
 XX PR Contreras RH, Nelissen B, De Backer MD, Luyten WHML, Viaene JE;
 PI Loghe MG;
 XX WPT; 2000-258614/23.
 XX PR Essential polypeptides isolated from *Candida albicans*, useful in the
 treatment of diseases caused by *C.albicans*, especially in
 immunocompromised subjects, e.g., AIDS patients -
 XX PS Claim 33: Figure 29; 133pp; English.
 XX This sequence represents a polypeptide that is critical for the survival
 CC and growth of *Candida albicans*. The *C. albicans* nucleic acid molecules
 CC encoding the polypeptides of the invention may be used as probes and
 CC primers for detecting homologous nucleic acid molecule sequences. The
 CC polypeptides and nucleic acid molecules and compounds identified as
 CC selectively modulating the expression of the polypeptides, may be used as
 CC medicaments or for the preparation of a medicament to treat *C. albicans*
 CC associated diseases, especially in AIDS patients and to treat
 CC vulvovaginitis in otherwise healthy females. The use of the polypeptides
 CC and polynucleotide sequences to treat *C. albicans* associated diseases has
 CC fewer side effects and less toxicity than previously used methods such as
 CC the use of amphotericin. This method is therefore especially suitable for
 CC immunocompromised patients, such as AIDS patients.
 XX SQ Sequence 707 AA;

Query Match 11.8%; Score 85; DB 21; Length 707;

Best Local Similarity 22.3%; Pred. No. 5.8;
 Matches 33; Conservative 33; Mismatches 56; Indels 26; Gaps 7;

QY	6 AFVFFEDENLSSSGSIIHLEVKQNC-SPNYDYEKTFIDGYLYIKN-----KGIV 55
Db	357 SYLFNIDVKIKSKS---IQLVFNSTDONYHHTK----YFYTCKTRGPGSNYKGGA 406
OY	56 ILDKYDLKVISVALKRDYLSSLNSNKFI-KKEFKNIKHNKFLNKFNLVINYINEDIEKRI 114
Db	407 LMNKI--NKIHLSNNKPKPRHKRVSNNNRNYNKSLSKGVLHEKFDKNFVEYLSE-QRKY 461
OY	115 TKNGILEEVILNKMLSLILLGNEEMLAQ 142
Db	462 TEDYSNLEIHLNSLQFNVLNTYRGVAQ 489

Search completed: July 24, 2003, 20:05:59
 Job time : 113.273 secs

APPLICANT: Ledebotter, Adrianus M.
APPLICANT: Venema, Gerard
APPLICANT: Kok, Jan
TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid Bacterium for Production of Desired Protein
TITLE OF INVENTION: Bacterium, and Its Use in a Lactic Acid Bacterium for Production of Desired Protein
FILE REFERENCE: Sanders-60113/0252227
CURRENT APPLICATION NUMBER: US/09/068,195B
CURRENT FILING DATE: 1997-07-29
EARLIER APPLICATION NUMBER: PCT/EP97/04755
EARLIER FILING DATE: 1997-08-20
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER FILING DATE: 1997-03-13
EARLIER APPLICATION NUMBER: EP 96202444/4
EARLIER FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 297
TYPE: PRT
ORGANISM: *S. gorodni*
-09-068-195-12

Query Match	12.58	Score 90.5;	DB 3;	Length 297;
Best Local Similarity	24.58;	Pred. No.	0.06;	
Matches 39;	Conservative 31;	Mismatches	54:	Indels 35; Gaps 8;
5 QAFVFEDENLSSSGSSTHLEVKVKGNSPNDYFK - ITFIDGYLYIKNKSGVILDKYDL 62				
103 EAMAQEPEKKNYKLNTIVIATLTSCNPDYQSKGDFEFLTYLFSVEEMG -- -RYEL 158				
63 ---KVNISLVALK----- RDYLSLSLSNNKQIKFKN --- IKNHLK - N 99				
159 WLFTNSVNLTLTLETFFASEMINRTOFYNNLPNNRRRIKMLNNVYASCIENNHLQVAM 218				
100 KFNLYVINEDIKEKRITNGILEEVIL - NKMLLSILGN 136				
219 KFLNYL - - -TKIPETDLYDRVLYKHAKA - YSKYKVN 253				

SULT 3
-09-107-532A-4250
Sequence 4250, Application US/09107532A
Patent No. 6513275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FASCIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts

CONTRIB: USA
ZIP: 02554
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489

RESULT 5
US-08-286-325A-2
Sequence 2, Application US/08286325A
GENERAL INFORMATION:
Patent No. 5658770
APPLICANT: PREVOTS, Fabien
APPLICANT: REMY, Elisabeth
APPLICANT: RITZENTHALER, Paul
TITLE OF INVENTION: Nucleic acid sequence and plasmids comprising at least one phage resistance mechanism, bacteria in which they are present, and their use
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BACON & THOMAS
STREET: 625 Staters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,325A
FILING DATE: 04-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 09 777
FILING DATE: 09-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: FIGHTER, Richard E.
REGISTRATION NUMBER: REF/BEDL/
REFERENCE/DOCKET NUMBER: REF/BEDL/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 540 amino acids
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-286-325A-2

Query Match 11.18; Score 80.5; DB 1; Length 540;
Best Local Similarity 22.9%; Pred. No. 1.7;
Matches 32; Conservative 21; Mismatches 52; Indels 35; Gaps 4;

Qy 4 KQAFVFEFDENLSS--SGSIHLKVKQNCSPNVDYKTFIDGYLYIKNKSCVILDKY 60
Db .98 KEPDLRFGNYSIELSKTTVEAQKQQLCKVYFLN-----FUSTKTRVISTSP 149
Qy 61 DLKNVISVALKRDYLSSL-----NNQIKKKFKNIK-----KH 96
Db 150 DISSYYIPSENKYINSLCTECDIILQKEFLYNTKEVDSFFDIKYLVSPNDVEKF 209

Qy 97 LKNKPNLYVINEDIEKRITK 116
Db 210 LDDKYFLTPHQDQIVKITE 229

RESULT 6
US-09-134-001C-3411
Sequence 3411, Application US/09134001C
GENERAL INFORMATION:
Patent No. 6380370
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
NUMBER OF SEQ ID NOS.: 5674
SEQ ID NO: 3411
LENGTH: 183
TYPE: PRT
ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-3411

Query Match 11.0%; Score 79.5; DB 4; Length 183;
Best Local Similarity 22.7%; Pred. No. 0.48;
Matches 32; Conservative 27; Mismatches 51; Indels 31; Gaps 5;

Qy 2 ELKQAFVFEFDENLSSGSSTHLEKVKQNCSPNVDYKTFIDGYLYIKNKSCVILDKY 61
Db 30 DLSQGYISQLESNAHSPSMETFLNIEVLGTSASDFKEPSDEKVLYKKEQTIVDEID 88

Qy 62 LKNVTS-LVALKRDY---LSLSLNNKQIKKKFKNIKHLKKNFNLVYVINEDIEKRITK 116
Db 89 KGYTLNWLYANSNFDMPEPILTTRPNSAYKNEPKSESDTF----TYCLNGEV---- 137

Qy 117 NGILEEVILNKMLLSILLGNE 137
Db 138 -----SLQLGNO 144

RESULT 7
US-08-645-193B-15
Sequence 15, Application US/08645193B
Patent No. 5962253
GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Gotz, Friedrich
APPLICANT: Kempfer, Christoph
APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,193B
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1540000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-645-193B-15

Query Match 10.9%; Score 79; DB 2; Length 990;
 Best Local Similarity 24.3%; Pred. No. 5.7;
 Matches 37; Conservative 25; Mismatches 46; Indels 44; Gaps 8;

Qy 2 ELKQFVFERDENLSSSGSITHLEVKQNCSPNYDFKTFIDGYIKNSGVILDKYD 61
 Db 315 ELKQSLA---DNIEAAAYIWL-----LSPNH-----FCTKTFNYHEFFMDKY 356

Qy 62 LKNVISLVAL-----KRDYLISLSNKKOKKFKNI----KXKHLKXNKPNFLYYN 107
 Db 357 FEQLVNKLQKLDINGFGYPKKD-SYSPSNTIAFLKEVYLLAONNSHIE----IT 407

Qy 108 EDIERKRITNGILEFY---ILNKMLISILGN 136
 Db 408 ENDVRLNEKNTVSKINAPVSTEYSEIYFGN 439

RESULT 8 PCT US93-07261-11

Sequence 11, Application PC/TUS9307261

GENERAL INFORMATION:
 TITLE OF INVENTION: PFEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF
 NUMBER OF SEQUENCES: 23CORRESPONDENCE ADDRESS:
 ADDRESSEE: John H. C. Blasdale

STREET: One Girarda Farms

CITY: Madison

STATE: New Jersey

COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE FORM:

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07261

FILING DATE: 19930805

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/927,531

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.

REGISTRATION NUMBER: 31,895

REFERENCE/DOCKET NUMBER: DX0288K

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7398

TELEFAX: 201-822-7039

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1663 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Plasmodium falciparum

STRAIN: Malayan Camp

PCT-US93-07261-16

RESULT 10 US-09-328-352-6424

Sequence 6424, Application US/09328352

GENERAL INFORMATION:

PATENT NO: 6562058

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBAC

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: GTC59-03PA

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO: 6424

LENGTH: 411

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-6424

RESULT 9 PCT-US93-07261-16

Sequence 16, Application PC/TUS9307261

QY 36 DFKITFIDCYIKNKSGVILDKYDVLKVNISVALKKRDLVLSLSNKQIKKFKN--IK 93
 1| 1| 1| 1| 1| 1| 1| 1| 1| 1| 1| 1| 1| 1|
 Db 60 DYEKITLEDARILAQK-----LKEI-----TDSNPLSKNNKLTKNSUNEKID 103
 QY 94 NKHILKRNKFNLVINYNEDEIKRITKN---GILBEVILNKMLLISL---LGNBENLLOIS 144
 Db 104 QPYLKEAFQVYINHHELKERTLADYREVIEKYLIDLSLEKLIDTEQREEKYIQLS 160

RESULT 11
 US-09-770-170-8
 Sequence 8, Application US/09770170
 Patent No. 6319619
 GENERAL INFORMATION:
 APPLICANT: McKnight, Steven
 APPLICANT: Gardner, Kevin
 APPLICANT: Harper, Shannon
 APPLICANT: Rutter, Jared
 APPLICANT: Michnoff, Carolyn
 APPLICANT: Amezcua, Carlos
 TITLE OF INVENTION: PAS Kinase
 FILE REFERENCE: UMSD-0761
 CURRENT APPLICATION NUMBER: US/09/770,170
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 8
 LENGTH: 1101
 TYPE: PRT
 ORGANISM: yeast
 CURRENT FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 8
 LENGTH: 1101

Query Match 10 7% Score 77; DB 4; Length 1101;
 Best Local Similarity 19.3%; Pred. No. 11; Indels 52; Gaps 9;
 Matches 39; Conservative 39; Mismatches 52;

QY 13 ENLSSSSGSIHLKEYKQ-----NCSPNYDVKITPIDE-----YL 47
 Db 712 ETISNSDDEVLDNQVNEKLRETSCGKVRGIESNDNNYD-DDMTWVDPELKHKTELTKM 770

QY 48 YIKNKGVIDL---KYDVLKVNISLV-----ALKRDYLS---LSLS 81
 Db 771 YTQDKSKFVKDDNFKVDEKFIMRITEPINGEEIKKETNEDLKRNSTLKATLTPEANIG 830

QY 82 NNKQIKKFKN----TKNKLKKNKFNLVYINED---IEKRITKNGLLEVLN---- 126
 Db 831 SQKRKFKFSDETLQMGEGAYKVNLCIHNRHYTIVKMFKERILVDTWDRKLG7 890

QY 127 ----KMLLSLILGNEBNLLOI 143
 Db 891 IPSEIQIMATLNKNSQNILKL 9f2

RESULT 12
 US/08-021-601-12
 Sequence 12, Application US/08021601
 Patent. No. 5591631
 GENERAL INFORMATION:
 APPLICANT: Leppla, Stephen H.
 APPLICANT: Klimpel, Kurt R.
 APPLICANT: Nichois, Peter J.
 APPLICANT: Arora, Naveen
 APPLICANT: Singh, Yogendra
 TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND RELATED METHODS
 NUMBER OF SEQUENCES: 12

ADDRESSEE: Needle & Rosenberg, P.C.
 STREET: 133 Carnegie Way, Suite 400
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA

ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/021-601
 FILING DATE: 19930212
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Spratt, Gwendolyn D.
 REGISTRATION NUMBER: 36 016
 REFERENCE/DOCKET NUMBER: 1414 057
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404/688-0770
 TELEX/FAX: 404/688-9880
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 903 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-021-601-12

Query Match 10.6% Score 76.5; DB 1; Length 903;
 Best Local Similarity 20.6%; Pred. No. 9.4;
 Matches 42; Conservative 33; Mismatches 50; Indels 79; Gaps 11;

Qy 7 FVFEFDENLSS-----SSGITH--LEVKVQNCSPN-----YDFKTT-----41
 Db 550 FDFNFQDTSNIKNOELAELNATIYVLDIKLNAKMNLIRDQRFHYDRNNIAVGAE 609

Qy 42 -----FIDGY LY -IKNKG-----VILDKYDLKAVNISLV 69
 Db 610 SVVKEAHREVINSTEGLLNIDKDIRKLSGYTIVEDFEGLKVEYINDRMLNSSL- 668

Qy 70 ALKDYLSSLISLNKQIKKFKNKNK--HLKN--KFNLYVINEDEIKR----TKNGIL 120
 Db 669 -----RQDGKTFIDFKYNDLPLVTSNPVNVKVNYYAVTK--ENTLINSENGDT 716

Qy 121 BEVILNRMLLSILGNEBNLLOI 144
 Db 717 STNGIKKILKKVVLGKGDTWELT 740

RESULT 13
 US-08-082-849B-12
 Sequence 12, Application US/08082849B
 Patent. No. 5677274
 GENERAL INFORMATION:
 APPLICANT: Leppla, Stephen H.
 APPLICANT: Klimpel, Kurt R.
 APPLICANT: Arora, Naveen
 APPLICANT: Singh, Yogendra
 APPLICANT: Nichois, Peter J.
 TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and Related Methods
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/082-849B

FILING DATE: 25-JUN-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/021,601
 FILING DATE: 12-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 31,677
 REFERENCE/DOCKET NUMBER: 15280-161-1
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 903 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-082-849B-12

Query Match 10 68; Score 76.5; DB 1; Length 903;
 Best Local Similarity 20.68; Pred. No. 9.4; Gaps 11;
 Matches 42; Conservative 33; Mismatches 50; Indels 79; Gaps 11;
 Qy 7 FVFEFDENLSS-----SSGSIH--LEVKVONCSPN-----YDYFKIT---- 41
 Db 550 FDFNFDQQTSONQNQALNATNITYVLDKIKUNAKUNILIRDKRFHYDRNNIAVGADE 609

Query Match 10 68; Score 76.5; DB 1; Length 903;
 Best Local Similarity 20.68; Pred. No. 9.4; Gaps 11;
 Matches 42; Conservative 33; Mismatches 50; Indels 79; Gaps 11;
 Qy 7 FVFEFDENLSS-----SSGSIH--LEVKVONCSPN-----YDYFKIT---- 41
 Db 550 FDFNFDQQTSONQNQALNATNITYVLDKIKUNAKUNILIRDKRFHYDRNNIAVGADE 609
 Qy 42 -----FIDGYLY-IKNGSG--VILDKYDLKNVISLV 69
 Db 610 SVVKEAHREVINSSTEGLLNIKDIRKLISGYIVEIEDTEGLKEVINDRYDMNINSSL- 668
 Qy 70 ALKDYLDSLNSNKKQ1KKFKNKNK--HLKN--KFNLVYVINEDIEKRI---TKNGTL 120
 Db 669 -----RDGRTFIDKNDKPLIYISNPNKVNVAVTK--ENTIINPSENEDT 716
 Qy 121 EEVINKMLLSILLGNEENLLOIS 144
 Db 717 STNGTKKILKVVILGGKGDTVELT 740
 RESULT 15
 Sequence 3, Application US/09437277
 ; Sequence 3, Application US/09437277
 ; General Information:
 ; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
 ; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
 ; FILE REFERENCE: 5820_551
 ; CURRENT APPLICATION NUMBER: US/09/437,277
 ; CURRENT FILING DATE: 1999-11-10
 ; NUMBER OF SEQ ID NOS: 6
 ; SEQ ID NO 3
 ; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
 ; LENGTH: 965
 ; TYPE: PRT
 ; ORGANISM: Pasteurella multocida
 US-09-437-277-3

Query Match 10 68; Score 76.5; DB 4; Length 965;
 Best Local Similarity 25.58; Pred. No. 10; Gaps 4;
 Matches 28; Conservative 27; Mismatches 44; Indels 11; Gaps 4;
 Qy 35 YDYFKITFID-GLYTIKNGSGVILDKYDLKNVISLVAKRDYLSL-----SNKKQ1KKF 89
 Db 664 YNYDKFDIDDESRYIFNKTAEQEMMLKDJLQIQNDKAIASIFYPTNLGLYKRL 723
 Qy 90 KNIKMKHLKNKFNLVYVINEDIEKRTKNGILEEVI-LNKMLLSILLGNE 137
 Db 724 NNI---IYEYKNNFVILLHVDNHNHLPDIKEFLAFHKHQVNNILAND 769
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/01624
 FILING DATE: June 25, 1993
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 31,677

Search completed: July 24, 2003, 20:09:25
 Job time : 40.3377 secs

RESULT 2
US-09-950-041-37
Sequence 37, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastellein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
SEQ ID NO: 37
LENGTH: 1032
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (725),(725)
OTHER INFORMATION: The 'xaa' at location 725 stands for Ile.

US-09-950-041-37

Query Match 11.3%; Score 81.5; DB 11; Length 1032;
Best Local Similarity 25.5%; Pred. No. 10;
Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

Qy 1 MELKQAFVFEFDENLSSGSSGSIHLKYKQNCSPNYDFK-----ITFIDG-YLYIK 50
Db 59 LDLSDNFITHIN -ESFGQLQNLTKINLNHNPWVQHONGNPQTQNSGUNITDGAFLNK 116
Qy 51 NKSSVILQKYDLKNV1SVALKRDYLSLSLNN-----KQIKKFKNKHNKLNKFN 103
Db 117 NLRELLNEQLPQPS -GLPESLTSLQNNIYTKEGISRLNKLNLYL-AWNC 172
Qy 104 YVINEDIEKRITNGILEEVILNMLLSI 132
Db 173 Y-FNKVCEXTNIEDGVF-ETLTNLSSL 199

RESULT 3
US-09-864-761-38325
Sequence 38325, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

RESULT 4
US-09-378-295A-498
Sequence 498, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillian, Kenneth J.
 ; APPLICANT: Kjavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paonzi, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Sheldon, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/063250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077641
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077649
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077791
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/078004
 ; PRIOR FILING DATE: 1998-03-13
 ; PRIOR APPLICATION NUMBER: 60/078886
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078936
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR APPLICATION NUMBER: 60/079556
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079664
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079889
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079663
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079786
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079920
 ; PRIOR FILING DATE: 1998-03-30
 ; PRIOR FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 60/080105
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080107
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080165
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080194
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080327
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080328
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081071
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081819
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081952
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-23
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/083392
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083496
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083499
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/0835554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/0835558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/0835559
 PRIOR FILING DATE: 1998-04-29
 PRIOR FILING NUMBER: 60/0835000
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/0837442
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/0843666
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/0844144
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/0844441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/0846337
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/0846339
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/0844440
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/0853339.
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/0853338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/0855882
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/0857000
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/0855579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/0855880
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.38; Score 25.58; Pred: Mi
 Best Local Similarity 25.58; Conservative 25; Mi
 Matches 38; Conservative 25; Mi

1 MELKOAFYFEDENLSSSSGSIH
 :: : | : | : | : | : | : |
 68 LDLSDNFTHTIN--ESFGQLQNLT

51 NKGSVILDKYDLKVNIVSVALVKRDY
 | : | : | : | : | : | : |
 182 Y-FNKQCEKFTNEDGEFETTUNPFR

104 YVINEDLEKRITKNGTILEBEVLNKM
 126 NRRELIEDNOLPQIOPPS--GLPESSL

Query Match Score 81.5; DB 10;
Best Local Similarity Pred. No. 10;
Length 1041;

GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Oiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goodard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Kijaviv, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James;
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Shelton, David L.
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Willians, P. Mickey
 / APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE NUMBER: Acids Encoding the Same
FILE REFERENCE: P2630PC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066564
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079339
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079556
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663

```

; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/0801070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082200
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084457
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084644
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084645
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085589
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.3%; Score 81.5%; DB 10; Length 1041;
Best Local Similarity 25.5%; Pred. No. 10;
Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

Qy      1 MEIJKQAFYEFDEFDNLSLSSGSIHLKVQNCSPNYDFK-----ITFIDG-YLYIK 50
Db      68 LDDSDNFITHIN -ESFOGLQLNTKINLNHNENVQHONGNPQISNGNLNTGAFNLK 125
Qy      51 NKSGVILDKYDLKVNISLVALKDYLSSLNN-----KQTKFKNKNKLNKFNKL 103
Db      126 NURELLIEDNOLEPQIPS -GLPESLTSLIQNNYNTKEGISRLNLKNLNLW-AWNC 181

Qy      104 YVINEDIEKRITNGILBEVLKMLISI 132
Db      182 Y-FNKVCEKTNIEDGVF-ETLTNLLELSL 208

RESULT 6
US-09-978-192A-438
; Sequence 498, Application US/09978192A

```

Patent No. US2002017753A1
 GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerter, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillian, Kenneth J.
 ; APPLICANT: Klijavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Sheldon, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumans, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C9
 CURRENT APPLICATION NUMBER: US09/978,192A
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR APPLICATION NUMBER: 60/077804
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080328
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080335
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080336
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080337
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080338
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081819
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081952
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085382
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.3% Score 81.5; DB 10; Length 1041;
Best Local Similarity 25.5%; Pred. No. 10;
Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

1 MELKQAFYFFEDNLSLSSSGSITHLEWKQNSPQNYDFK-----ITFIDG-YLYIK 50
68 LDLSDNFIHTHIN - ESGQLQNLTKINLNHNPKVQHQNGNPQIOSNGLNTDGAFLNLK 125
51 NKGVIDKDLYKLNVISLVALKRDYLSSLSSNN-----KOIKKPRNIKUHKLHNFNL 103
DB 126 NURELIEDNOLPQIS - GLPESLTPLSLQNNIYNTKREGISRLINLKLYL - AWNC 181

Oy 104 YVINEDIKRITKNGILEEVILNKMLSI 132
Oy 182 Y-FNKVCEKTNIEDGVF-ETLTNLELLSL 208

RESULT 7
US-09-999-832A-498

Sequence 498, Application US/09999832A
Publication No. US200192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Kijavim, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Sheldon, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS Encoding the Same
FILE REFERENCE: P2630PIG163
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918385
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077532
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077911
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078946
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079394
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079566
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081819
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081952
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083500
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match Score 81.5; DB 10;
 Best Local Similarity 11.3%; Pred. No. 10;
 Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

Qy 1 MELKCAFVFFDENLSSSGSIILEVKONCSPNYDFK-----ITFIDG-YLYIK 50
 Db 68 LDLSDNFIHTIN--ESFGQLNLTKINHNPVHQHNGPQSNGNUTDAGLNK 125
 Qy 51 NKSGVILDKYDKNVISVALKDYLTSLSNN-----KQIKFKNKNKHLKKNKFNL 103
 Db 126 NLRELLDNQPOIPS--GLPESLTTELSONNNNTKEGRSLNKLNL--ANNC 181
 Qy 104 YVINEDIEKRTKNSILEEYLNKMLSI 132
 Db 182 Y-FNKVCEKTNIEDGVF-EVLTNLELSSL 208

US-09-978-189-498 Application US/09978189
; Sequence 498, Application US/09978189
; Publication No. US200300041022A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillian, Kenneth J.
; APPLICANT: Klijavins, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William J.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC7
; CURRENT APPLICATION NUMBER: US/09-978-189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27 ; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27 ; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27 ; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27 ; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30 ; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30 ; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31 ; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31 ; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31 ; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-03-31 ; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31 ; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080335
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080336
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080337
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080338
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080339
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080340
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080341
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080342
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080343
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080344
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080345
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080346
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080347
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080348
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080349
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080350
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080351
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080352
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080353
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080354
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080355
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080356
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080357
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080358
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080359
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080360
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080361
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080362
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080363
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080364
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080365
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080366
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080367
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080368
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080369
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080370
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080371
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080372
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080373
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080374
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080375
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080376
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080377
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080378
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080379
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080380
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080381
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080382
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080383
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080384
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080385
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080386
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080387
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080388
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080389
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080390
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080391
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080392
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080393
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080394
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080395
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080396
; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080397

```

; PRIORITY APPLICATION NUMBER: 60/083499
; PRIORITY FILING DATE: 1998-04-29
; PRIORITY APPLICATION NUMBER: 60/083545
; PRIORITY FILING DATE: 1998-04-29
; PRIORITY APPLICATION NUMBER: 60/083554
; PRIORITY FILING DATE: 1998-04-29
; PRIORITY APPLICATION NUMBER: 60/083558
; PRIORITY FILING DATE: 1998-04-29
; PRIORITY APPLICATION NUMBER: 60/083559
; PRIORITY FILING DATE: 1998-04-29
; PRIORITY APPLICATION NUMBER: 60/083560
; PRIORITY FILING DATE: 1998-04-29
; PRIORITY APPLICATION NUMBER: 60/083742
; PRIORITY FILING DATE: 1998-04-30
; PRIORITY APPLICATION NUMBER: 60/084366
; PRIORITY FILING DATE: 1998-05-05
; PRIORITY APPLICATION NUMBER: 60/084414
; PRIORITY FILING DATE: 1998-05-06
; PRIORITY APPLICATION NUMBER: 60/084441
; PRIORITY FILING DATE: 1998-05-06
; PRIORITY APPLICATION NUMBER: 60/084637
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/084639
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/084640
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/084598
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/084600
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/084627
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/084643
; PRIORITY FILING DATE: 1998-05-07
; PRIORITY APPLICATION NUMBER: 60/085339
; PRIORITY FILING DATE: 1998-05-13
; PRIORITY APPLICATION NUMBER: 60/085338
; PRIORITY FILING DATE: 1998-05-13
; PRIORITY APPLICATION NUMBER: 60/085323
; PRIORITY FILING DATE: 1998-05-13
; PRIORITY APPLICATION NUMBER: 60/085582
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085700
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085689
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085579
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085580
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085573
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085704
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085697

Query Match 11.3%; Score: 25.5%; Pred: Matches 38; Conservative 25; Min: 1
Best Local Similarity 25.5%; Pred: Matches 38; Conservative 25; Min: 1

```

RESULT 9
US-09-978-608A-498
; Sequence 498, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flavroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillian, Kenneth J.
; APPLICANT: Kjavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paci, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Sheldon, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secred and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 498
; LENGTH: 1041
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-498

Query Match Score 81.5; Length 1041;
Best Local Similarity 25.5%; Pred. No. 10;
Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 0

Qy 1 MELKQAFYFEEFDENLSSSSGSIILEVKVQNCSPNYDVFK-----ITFDG-YLYIK S
Db 68 LDLSBDSNFIITHIN--ESFGQLNLTQKINLNHNPVYOHONGNPQIOSNGLNITDGAFLNK 1

Qy 51 NKSGVILDKDKVNTISLVALKDYLISLSNN-----KQIKKKNNKNNHLKNNFKNL 1
Db 126 NLREILLEDNOLPQIPS--GLPESTELSLUJONNNYTREGISRLNLKMYL-AWNC 1

Qy 104 YVINEDIEKRITKGNGILEEVILNKMLSI 132
Db 182 Y-FNKVCERTNIEDGVF-ETLNLLELISL 208

RESULT 10
US-09-978-585A-498
; Sequence 498, Application US/09978585A
; Publication No. US2003004963A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2610PIC4

CURRENT APPLICATION NUMBER: US/09/978,191A

CURRENT FILING DATE: 2001-10-15

NUMBER OF SEQ ID NOS: 624

PRIOR APPLICATION removed - See File Wrapper or Patm

SEQ ID NO: 498
 LENGTH: 1041
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-978-585A-498

Query Match 11.38; Score 81.5; DB 11; Length 1041;
 Best Local Similarity 25.5%; Pred. No. 10;
 Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

Oy 1 MELKQAFVFERDENLSSSSSIHLERVKQNCSPPNYDFK-----ITFIDG-YLYIK 50
 Db 68 LDLSDNFITHTN- -ESFGQLQNLTKINLNKRDYLSSLSSNN-----KOIKKFKNKTKNHLKFNKL 125
 Oy 51 NKGSYTLDKYDKNVISVALKRDYLSSLSSNN-----KOIKKFKNKTKNHLKFNKL 103
 Db 126 NLRELLEDNOLPQIPS--GLPESLTLSLQNNIYNTRKEGTSRNLKNLYL--AWNC 181

Qy 104 YVINEDIEKRITKNGILEEVILNKMLLSI 132
 Db 182 Y-FNPKVCEKTNIEDGVF-ETLTLNLELLSL 208

RESULT 11
 US-09-978-191A-498
 Sequence 498, Application US/09978191A
 Publication No. US20030050239A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Klijavin, Ivar J.

PRIOR APPLICATION NUMBER: 60/080323
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083396
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083395
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083399
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06

```

; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085333
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15

Query Match 11 : 38 ; Score 81.5 ; DB 11 ; Length 104;
Best Local Similarity 25.5% ; Pred. No. 10;
Matches 38 ; Conservative 25 ; Mismatches 61 ; Indels 25 ;
Gaps 8;

Qy 1 MELKAFVFFEDNLNLSLSSGGSHILEVKONCSPNYDYFK-----ITFIDG-YLYIK 50
Db 68 LDLSDNFIHTHN- EFSFQLQNLTKINUHNPNVOHONGNPQTOSNGNUNITDGAFLNKJ 125
Qy 51 NKGSVYLDKYDLKNVISLYALKRDYLSLISLSSNN-----KOIKKFKNKNIKHLKKNKFNL 103
Db 126 NLREILLEDNQLPQPS- GLPESTELSLIUNNYYNTKEGISRLLNLKLYL- ANWC 181
Qy 104 YVINEDEIEKRTPQGLEEVYLKNMDSL 132
Db 182 Y-FNWKVEKTNIEDGVF-EPLTNLLELLSL 208

RESULT 12
US-09-978-403A-498
; Sequence 498, Application US/09978403A
; Publication No. US2003005040A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hans Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillman, Kenneth J.

```

APPLICANT: Kjavian, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C17
 CURRENT FILING DATE: US/09/978,403A
 CURRENT FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249.
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327

; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080328
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081071
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081819
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081952
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082700
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-23
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083495
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083496
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083499
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083500
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083558
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 11 3%; Score 81.5; DB 11; Length 1041;
 Best Local Similarity 25.5%; Pred. No. 10;
 Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

Qy	1 MELKQAFVFPDENLSSSGSSSIHLKEVKQNCSPNVDYFK-----ITFIDG-YLYIK 50
Db	68 LDLSDNFIHTHN--ESFOGLQNLTKINLHNPNVQHQNNGPQGSNGLNITDGFNLNK 125
Qy	51 NRSGVILDKYIKNVSLVAIKRDLTSLSNN-----KOIKFKNIKHKLNKFNFL 103
Db	126 NLRELLEDNOLPQIS--GLPESLTLSLQNNYNTREGISRLNKLNL--AWNC 181
Qy	104 YVINEDTEKRITKGTLVEEVILNKMLSI 132
Db	182 Y-FNKVCEKTNEEDGVF-ETLTNLEDLSL 208

RESULT 13
 US-09-546-136-5.rappb
 Sequence 498, Application US/09978564A
 Publication No. US20030050241A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.

APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kjavian, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tunas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey
 TITLE OF INVENTION: Secred and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C25
 CURRENT APPLICATION NUMBER: US/09/978,564A
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 09/18585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31

```

; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441

PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084650
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085574
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579

Query Match 11.3%; Score 81.5%; DB 11; Length 1041;
Best Local Similarity 25.5%; Pred. No. 10; Mismatches 61; Indels 25; Gaps 8;
Matches 38; Conservative 25; MisMatches 61; Indels 25; Gaps 8;

Qy 1 MEUKQAFVFFEDNLSSSGSITHLEKYKQNCSPNYDFK-----ITFIDG-YLYIK 50
Db 68 LLDSDNFTHITN--ESFGQLQNLTKINLNHNPVNQHQNGNPQISQNSGLNTIDGFLNK 125
Qy 51 NKGSVILDKYDILKNVISVALKRDYLSLSSLNN-----KOIKPKNIKHNKHNKFNL 103
Db 126 NLRELLDNQLEQIPS--GLPESLTTELSONIINYITKEGISRNLNKLNL--AWNC 181
Qy 104 YVINEDIEKRITKINGILEEVILNKMLSLI 132
Db 182 Y-FNKVCETKNEIDGVF-ETLNELLSL 208

RESULT 14
US-09-99-833A-498
; Sequence 498, Application US/09999833A
; Publication No. US20030054405A1

GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

```

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Klijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2630PIC65
CURRENT APPLICATION NUMBER: US/09/999-833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918565
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/067450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194


```

; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match Score 11.38; Score 81.5; DB 11; Length 1041;
Best Local Similarity 25.5%; Pred. No. 10;
Matches 38; Conservative 25; Mismatches 61; Indels 25; Gaps 8;

QY 1 MELKOAFYFEPFDENLSSSGSISLEKVKONCSPNYDFK-----ITFIDS-YLYIK 50
Db 68 LDLSDNFITHTN - ESEFGLOQNITKINLNHNPVQHONGNPGIOSNLNTGAFNLN 125
QY 51 NKSGVILDKYDLKAVISVALKDYLSSNN-----KQIKKFKNKHNKHNKHNKL 103
Db 126 NLRELLLEDNQLPOIPS --GLPESITESLQNNIYTKEGSRLINKNKL - ANNC 181
QY 104 YVNNDIEKRITKNGILEEVLNRMLLSI 132
Db 182 Y-FNKVCERTNIEDGVF-ETLTNDELLSL 208

Search completed: July 24, 2003, 20:21:04
Job time : 65.7143 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 20:04:00 : Search time 46.7532 Seconds
(without alignments)
296.200 Million cell updates/sec

Title: US-09-546-136-5
Perfect score: 723
Sequence: 1 MELKQAFVFEFDEDNLSSSG LNKMLLSILGNENNLQIS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*

1: pir1:
2: pir2:
3: pir3:
4: pir4:
5:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	109.5	15.1	902	2	D84970	ribonuclease E (im type III restriction endonuclease)
2	104.5	14.5	1001	2	H64593	ribonuclease E (im type III restriction endonuclease)
3	101.	14.0	651	2	F90111	DNA primase (importin)
4	98.5	13.6	371	2	A64481	hypothetical prote
5	98.5	13.6	1039	2	S65059	probable vesicular protein
6	98.5	13.6	1044	2	T50213	probable vesicular protein
7	96.5	13.3	1224	2	E71611	hypothetical prote
8	95	13.1	404	2	F71718	alanine racemase (hypothetical prote)
9	94.5	13.0	2166	2	T28160	hypothetical prote
10	94	13.0	2166	2	G70163	ORF MSV251 hypothesized gene
11	92.5	12.8	329	2	T28412	hypothetical prote
12	92	12.7	602	2	E30568	DNA primase (importin)
13	92	12.7	2269	2	T18472	alanine racemase (hypothetical prote)
14	91	12.6	377	2	G65937	lipopolysaccharide
15	91	12.6	1183	2	F90559	conserved hypothetical prote
16	90.5	12.5	214	2	E90512	hypothetical prote
17	90.5	12.5	255	2	F89775	hypothetical prote
18	90.5	12.5	297	2	A1898	positive regulator
19	90.5	12.5	949	2	F90086	chromosomal region
20	89.5	12.4	714	2	C90100	hypothetical prote
21	89.5	12.4	786	2	T18469	hypothetical prote
22	89.5	12.4	3724	2	T18427	hypothetical prote
23	89	12.3	862	2	C9343	hypothetical prote
24	88.5	12.2	1247	2	E71616	hypothetical prote
25	88	12.2	498	2	B97046	hypothetical prote
26	88	12.2	1650	2	T18444	hypothetical prote
27	87.5	12.1	159	2	S26843	olfactory mucosa protein
28	87.5	12.1	335	2	S27674	hypothetical prote
29	87.5	12.1	386	2	S58755	ribosomal protein

ALIGNMENTS

RESULT 1
D84970
ribonuclease E [Imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D84970
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera ssp.
A;Reference number: A84930;
A;Accession: D84970
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: rne; BU347

RESULT 1
D84970
ribonuclease E [Imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D84970
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera ssp.
A;Reference number: A84930;
A;Accession: D84970
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: rne; BU347

Query Match 15.1%; Score 109.5; DB 2; Length 902;
Best Local Similarity 28.6%; Pred. No. 0.6;
Matches 44; Conservative 26; Mismatches 55; Indels 29; Gaps 6;

Qy 10 EFDE...LSSSSGCGSHLEVKVKCONCSPNYDFKTFIDGYLYIKNK...-SGVILDKYDLKVN1 66
Db 544 EAQNELLKKNNNNNILLKVLSN-NRNRFIKFMKMTWFNSFFTKMLTSIFKKNTLKNT- 601
Qy 67 SLVALKRDLYDSLSSLNNKQIKKF-----KNIKNKHLKN-----KFN 102
Db 602 NNIFFPKKYYSSLNKKNNNNQKRVILSKLFEEANIEPLKNNKKLDTSSANYLYDNTIERKKN 661
Qy 103 LYVINEDIEKRITKNGILEEVTLNKMLSTILGN 136
Db 662 ITKNDLJQKNHENSYLVHLMRNVNININN 695

RESULT 2
H64593
type III restriction enzyme R protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Accession: H64593
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: H64593
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKee, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; PMID:97394467
A;Accession: H64593
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A; Residues: 1-1001 <TOM>
 A; Cross-references: GB:AE000572; GB:AEO00511; NID:g2313703; PIDN:AA007657..1; PIDN:9231371
 C; Genetics:
 A; Start codon: TTG

Query Match 14.5%; Score 104.5; DB 2; Length 1001;
 Best Local Similarity 37.0%; Pred. No. 1.7; Matches 34; Conservative 12; Mismatches 31; Indels 15; Gaps 4;

Qy 24 LEKVKONCSPNYDFKITF---IDGVLY--IKNKGVLKDLMNVISLVALKRDYLSS 78
 Db 118 LESVKONIRLTKDVFLEFKRHLKTTYEGVKSPSNII--NHYIKN-----QDELSV 167

Qy 79 SLSNKQIKKFKNIKNHLKKNFKNLYVINED 110
 Db 168 LLLTNSAIDKEGNILNKNSENLFNTKSIFENI 199

RESULT 3
 F90111
 DNA primase (imported) - Guillardia theta nucleomorph
 C; Species: nucleomorph Guillardia theta
 A; Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C; Accession: F90111
 R; Douglas, S.; Zauer, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
 Nature 410, 1091-1096, 2001
 A; Title: The highly reduced genome of an enslaved algal nucleus.
 A; Reference number: A99082; PMID:11323671
 A; Accession: F90111
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-651 <JON>
 A; Cross-references: GB:AJ010592; NID:g12580737; PIDN:CAC27055..1; GSPPDB:GN00151
 C; Genetics:
 A; Gene: putative N-terminal transit sequence
 A; Map Position: 2
 A; Genome: nucleomorph
 C; Keywords: nucleomorph

Query Match 14.0%; Score 101; DB 2; Length 651;
 Best Local Similarity 28.3%; Pred. No. 1.9; Matches 50; Conservative 27; Mismatches 56; Indels 40; Gaps 11;

Qy 2 ELRQAFYFEFLNSSLSSGSI---HLEKTKQ--NCSPNYDFKITFIDGYLYTKNKG 54
 Db 167 ETKFYMLYKF-RNLNSLJMKLNLGYSNKKIISQINQENHEYLRI-----LKTMTKY 219

Qy 55 VLDKYDLKVN-----SVALKRDYLSLSLSS-----NNKQIKKFKNIK-NKHILKNF 101
 Db 220 VVFDKINKKVVDIRFLNRLVPIRNYYCLTLGFARTINSKKIPYLNSKENKEKKKK 279

Qy 102 NLVYVINEDIEKRITK-----NIGLEEVIL--NMILSLU-LGNEENLLOI 143
 Db 280 ILF-SEEIKSNISLSSKCCCLICEGYLDLSITLFGONGIRFSVASIGGSSNNFOI 330

RESULT 4
 A64481
 hypothetical protein MJ1450 - Methanococcus jannaschii
 C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C; Accession: A64481
 R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.; Kirkness, E.F.; Weinstock, K.G.; Meirick, J.M.; Giodek, A.; Reich, C.I.; Overbeek, R.; Merrick, J.M.; Glodek, A.; Pearson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.; Species: Methanococcus jannaschii

Qy 122 EVLNKMLSLLGNBENLL 141
 Db 782 EAELSKKALNDNLGNKENI 801

RESULT 5
 S62509
 probable vesicular transport factor - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 21-Jan-2000
 C; Accession: S62509; T38504
 R; Jones, L.; Murphy, L.; McNeill, A.; Simpson, I.; Harris, D.
 submitted to the EMBL Data Library, October 1995
 A; Reference number: S62507
 A; Status: preliminary
 A; Accession: S62509
 A; Molecule type: DNA
 A; Residues: 1-1039 <JON>
 A; Cross-references: EMBL:266525; NID:g1044926; PIDN:CAA91425..1; PIDN:91044929
 R; Jones, L.; Murphy, L.; McNeill, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajand
 A; Submitted to the EMBL Data Library, October 1995
 A; Reference number: S62508
 A; Status: preliminary
 A; Accession: T38504
 A; Molecule type: DNA
 A; Residues: 1-1039 <J02>
 A; Cross-references: EMBL:266525; PIDN:CAA91425..1; GSPPDB:GN00066; SPDB:SPAC29E6..03C
 A; Experimental source: strain 972h.; cosmid c29E6
 C; Genetics:
 A; Gene: SPAC29E6..03C
 A; Map position: 1
 A; Introns: 56/3; 606/3

Query Match 13.6%; Score 98.5; DB 2; Length 1039;
 Best Local Similarity 27.9%; Pred. No. 5.1; Matches 39; Conservative 27; Mismatches 43; Indels 31; Gaps 8;

Qy 22 HLKEVKQNCSPNYDFKITFIDGYLYTKNKG----YIKKSGVILDKYDLKVNLSVALK-RDV 75
 Db 673 FELDTYKSNQSMEEPMQV-LREGHESEIKFEEISKLTKQLDDDIKNQFQIISRRNRDL 731

Qy 76 LSLSLSNNKQIKKFKNI-----KNNKLNKFNLYVINEDIEKRIT-----KNGILE 121
 Db 732 LS-----ELEKSKLNNSSALESKNKKLENDNL-LTEKLNNKNADESFRNTI-R 781

Qy 122 EVLNKMLSLLGNBENLL 141
 Db 782 EAELSKKALNDNLGNKENI 801

RESULT 6
 T50213
 probable vesicular transport factor [imported] - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C; Accession: T50213
 R; McBougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, I.
 submitted to the EMBL Data Library, January 2000
 A; Reference number: 225046
 A; Accession: T50213

RESULT 10

G70163 hypothetical protein BB0512 - Lyme disease spirochete
C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: G70163
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, B.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
A;Reference number: A70100; PMID:9065943; PMID:9403685
A;Accession: G70163
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: AF001153; GB:AE000783; NID:92688419; PIDN: AAC66876.1; PID:9268842
A;Experimental source: strain B31

Query Match 13 0%; Score 94; DB 2; Length 2166;
Best Local Similarity 25.5%; Pred. No. 27;
Matches 36; Conservative 22; Mismatches 61; Indels 22; Gaps 4;

Qy ||| 7 FVFFEDENLSSSSG----IHLERVKQNCSPPNYDFKTFIDGYLYIKRNKGVILDKYD 61
Db 1951 FYSSFDTSRYKSLSIESDQYKAKKEIADE----QRTILDNVERISNKESI---- 1999

Qy 62 LKNVISLVALKRDLSSLSSLNQKIKFKNPKNKLKNKFNLVYINEDIKRITNGTILE 121
Db 2000 LKSTTIESVDKAFDLI-----NEVERKFNNSLUSKESAKIQDNLKDBENVSSLNLNGLSE 2053

Qy 122 EVLNKMLLSTLGNFENLHQ 142
Db 2054 EVLNQNLKEMLDIENKLK 2074

RESULT 11

T28412 ORF MSV251 hypothetical protein containing C3H2C3 RING finger - *Melanoplus sanguinipes* ε
C;Species: *Melanoplus sanguinipes* entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T28412
R;Atonso, C.L.; Tuiman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of *Melanoplus sanguinipes* entomopoxvirus.
A;Reference number: Z20484; PMID:99102612; PMID:9847359
A;Accession: T28412
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-129 </FO>
A;Cross-references: EMBL:AF063866; NID:94049647; PIDN: AAC97727.1; PID:94049767
C;Genetics:
A;Note: MSV251

Query Match 12 0%; Score 92.5; DB 2; Length 329;
Best Local Similarity 27.0%; Pred. No. 4;
Matches 40; Conservative 23; Mismatches 60; Indels 25; Gaps 7;

Qy ||| 13 ENLSSSSGSIITLEKVKQNCSPPNYDFKTFIDGYLYIKRNKGVILDKYDKNVISVALK 72
Db 163 ENININTSLLH----NCS_NNELSNINCVDLSKYIDCENNYIIEITNNELFLNCIN 216

Qy 73 RDYLSLSSLNN_KOIKKKFKNIK---NKH----LKN--KFLNLYVI---NEDIEKR 113
Db 217 NPLKLTISYNNLKSFKDTNLEIYIFNEHELIINGIKNVTDRFLUKKIEVFNDIDCSI 276

Qy 114 ITKNGGLEEVLNKMLLSTLGNFENL 141
Db 277 CLDKGILYKTCNHTFHKECLNNNNNL 304

RESULT 12

E90568 DNA Primase [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)
C;Species: *Mycoplasma pulmonis*
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90568
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulmonis*
A;Reference number: A99512; PMID:11353084
A;Accession: E90568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-602 <KUR>
A;Cross-references: GB:AL445566; PID:914089867; PIDN: CAC13626.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_4530
A;Genetic code: SG3

Query Match 12.7%; Score 92; DB 2; Length 602;
Best Local Similarity 26.7%; Pred. No. 8.8;
Matches 40; Conservative 24; Mismatches 48; Indels 38; Gaps 8;

Qy ||| 12 DENLSSSSGSIITLEKVKQNCSPPNYDFKTFIDGYLYIKRNKGVILDKYDKNVISVAL 71
Db 338 DELLKOKGANFLKELIEKKPAID-----YL-----EFLTSKNNINNSELHSIF 384

Qy 72 RDYLSL-SLSSLNNKQIKKKFKNIKRNKHLKLN--KFLNLYV-----NEDIEKR ----- 114
Db 385 VNDFAPLSSONNIVDKEYNLMLMRHSINTRKFETYQNKYDRINQNSLQRFYBEPKQ 444

Qy 115 -----TKNGGLEEVLN--KMLLSILGN 136
Db 445 RKKANSREEIILKKQYQONLYVKKLSSLNSN 474

RESULT 13

T18472 hypothetical protein C0440c - malaria parasite (*Plasmodium falciparum*)
C;Species: *Plasmodium falciparum*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18472
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z18937
A;Accession: T18472
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-269 <LAW>
A;Cross-references: EMBL:AL008970; NID:e1407852; PID:e1332566; PIDN:CAA15615.1
C;Genetics:
A;Gene: C0440c
A;Map position: 3

Query Match 12.7%; Score 92; DB 2; Length 2269;
Best Local Similarity 24.9%; Pred. No. 40;
Matches 47; Conservative 27; Mismatches 57; Indels 58; Gaps 9;

Qy ||| 11 FDENLSSSSGSIITLEKVKQNCSPPNYDFKTFIDGYLYIKRNKGVILDKYDKNVISVAL 72
Db 1812 YEGNDSSSSMDNNKSKQMKMKCNLNFRSVLGFLSMCPCNFDTKRNLYDNOTADIVYC 1871

Qy 41 FIDGYLYIK-----NKSCLVLDKYDKNVISVAL-----ALKRDYLSLSSL 81
Db 1872 SID-YSYNTDTYTWNYTFTVLPKTYFLTFPLSS_PYHDNVIIQTRTNLYTSDILSLSIKF 1930

Qy 82 NPKQI---KIFKNIKRNKHLKFNFLYVINEDIK_RITKNGLE---EVILKMLSLILL 134
Db 1931 DSKEITLKNMKMKHNKNTNTNYDTNSTINNPNTKHDLRVNYLRYVMSKLLSLSL 1990

Qy 135 G-NEENLHQ 142

RESULT 14		Best Local Similarity 30.0%; Pred. No. 23; Mismatches 45; Conservative 22;		Indels 28; Gaps 8;	
Db	1991 SFNQEETQ 1999	Qy	12 DENISSLGGSTHLEVKQNCSPNIDYFKTF-----IDGLYI--KKNKGVILDK 59	Db	557 NNNSSSKSGNFFLELKNTNYFSNNNUISVGYSNLKHNLIDKRLVPVEKSAGNLKN 616
G69937	C:Species: Bacillus subtilis	Qy	557 YDLKAV----ISLVALKRDYLSLSLNQRQIKEFKFNKHNKHNKFENLYVINDEIEKRI 114	Db	60 YDLKAV----ISLVALKRDYLSLSLNQRQIKEFKFNKHNKHNKFENLYVINDEIEKRI 114
C:Accession: G69937	C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	Qy	617 YLKKNNFEESSISUSSYEEIVQWNKLLNL-EFENIKN--NKYNKKIF-DIENKM 669	Db	617 YLKKNNFEESSISUSSYEEIVQWNKLLNL-EFENIKN--NKYNKKIF-DIENKM 669
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.	Nature 390, 249-256, 1997	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, M.; Fuma, S.; Galizzi, A.; Gallerie, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, M.F.; Koetter, P.; Koningschein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parzo, V.; Pohl, T.M.; Portebeau, Rieger, M.; Rivolte, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaike, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Serov, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.	A:Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . A:Reference number: A69580; PMID:98044033; PMID:9384377	Db	Search completed: July 24, 2003, 20:10:26 Job time : 50.7532 secs		
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown	A:Cross-references: GB:Z99115; GB:AL009126; NID:92634478; PIDN:CAB14162.1; PID:92634664	Qy	617 YLKKNNFEESSISUSSYEEIVQWNKLLNL-EFENIKN--NKYNKKIF-DIENKM 669	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain 168	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: YP_1H	C:Superfamily: probable hexosyltransferase ytxN	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-377 <KUN>	A:Cross-references: G69937	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Accession: G69937	A:Title: The complete genome sequence of the murine respiratory pathogen <i>Mycoplasma pulm</i>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Molecule type: DNA	C:Species: Mycoplasma pulmonis	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Accession: F90559	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820 [imported]	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	C:Species: Mycoplasma pulmonis (strain UAB CT	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Accession: F90559	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
C:Genetics:	C:Genetics:	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Gene: MPPU_3820	A:Gene: MPPU_3820	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Status: preliminary	A:Status: preliminary	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Residues: 1-1183 <KUR>	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Cross-references: GB:AL45566; PMID:914089796; PIDN:CA13555.1; GSPDB:GN00153	A:Residues: 1-1183 <KUR>	Qy	115 TKNGILEEVILNKMLLSILGNEENULQIS 144	Db	670 DS--LSTYVDNKNKLISLL-DEEFLKIN 695
A:Experimental source: strain UAB CTIP	A:Residues: 1-1183 <KUR></				

4	82.5	11.4	503	1	SYK-BUCAP
5	82.5	11.4	1076	1	RPOB-ASTLO
6	82	11.3	336	1	YD48-METJA
7	82	11.3	453	1	TRME-WIGBR
8	82	11.3	474	1	Y381-BORBU
9	82	11.3	569	1	CYSPL-PLAFA
0	81.5	11.3	490	1	PIT-BUCAI
1	81.5	11.3	1041	1	HUNMAN
2	81.5	11.3	1155	1	ROM1-YEAST
3	81	11.2	598	1	TDPL-LAEEL
4	81	11.2	628	1	GIDA-WIGBR
5	81	11.2	1636	1	YN37-YEAST
6					

1 MELIORAR VEF DENLSSSSSS : ENMLLSILLGNEENLEOIS 144

scoring table: BLOSUM62 ALIGNMENTS
 gapop 10.0 , Gapext. 0.5
 searched : 127863 seqs, 47026705 residues
 total number of hits satisfying chosen parameters: 127863
 minimum DB seq length: 0 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 10⁸ Maximum Match 10⁸
 Listing first 45 summaries Swissprot: 41; *
 database : RNE_BUCAI STANDARD: PRT; 902 AA.
 RESULT 1
 RNE_BUCAI
 ID RNE_BUCAI
 AC P57429;
 DT 16-OCT-2001 (Rel. 4.0, Created)
 DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
 DT 16-OCT-2001 (Rel. 4.0, Last annotation update)
 DE Ribonuclease E (EC 3.1.4.-) (RNase E).
 GN RNE OR BU347
 OS Buchnera aphidicola (subsp. *Acyrrhosiphon pisum*) (*Acyrrhosiphon pisum* symbiotic bacterium).
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OC

סימן זעמן

ALIGNMENTS					
RESULT 1					
RNE_BUCAI	ID	RNE_BUCAI	STANDARD:	PRT:	902 AA.
AC	P57429,				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Ribonuclease E (EC 3.1.4.-)	(RNase E).			
GN	RNE OR BU347.				
OS	Buchnera aphidicola (subsp. <i>Acyrtosiphon pisum</i>) (Acyrthosiphon pisum symbiotic bacterium).				
OS	Bacteria; proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera.				
OC					
OC					

SUMMARIES						
result No.	Score	Query Match	Length	DB ID	Description	
1	109.5	15.1	902	1 RNE_BUCA1	P57129 buchnera ap	
2	98.5	13.6	1044	.1 YAF3_SCIP0	009857 schizosacch	
3	95.5	13.2	650	1 MTLR_STRMU	002425 streptococc	
4	95	13.1	404	1 ALR_RICCP0	092652 rickettsia	
5	92	12.7	602	1 PRIM_MYCP0	Q984b3 mycoplasma	
6	92	12.7	873	1 SYA_WIGBR	Q8d288 wiggleswort	
7	91	12.6	377	1 YPJH_BACSU	P42982 bacillus su	
8	90.5	12.5	297	1 RGG_STRGCC	P49310 streptococc	
9	90	12.5	453	1 ENGA_BUCA1	051081 buchnera ap	
10	89.5	12.4	799	1 SYL_MYCP0	Q8ew18 mycoplasma	
11	87.5	12.1	159	1 OBP_BOVIN	P07415 bovis taurus	
12	87	12.1	386	1 RMAR_WANWI	P48849 hansenula w	
13	87	12.0	355	1 ALR_RICCN	Q92d19 rickettsia	
14	87	12.0	575	1 RPOC_ASTLO	P5b131 astasia lon	
15	87	12.0	811	1 RPOP_NEUNI	P33541 neurospora	
16	86.5	12.0	620	1 Y241_MYCGE	P47193 mycoplasma	
17	86	11.9	198	1 ENGB_CAME0	Ophph17 campylobact	
18	86	11.9	206	1 LOLA_WIGBR	P8d264 wiggleswort	
19	86	11.9	442	1 TIG_BUCA1	P757546 buchnera ap	
20	85.5	11.8	380	1 RMAR_NLMR	P47906 williopsis	
21	85.5	11.8	1155	1 IF2P_METJA	Q57710 methanococc	
22	85	11.8	414	1 YR28_BORBU	050999 borrelia bu	
23	85	11.8	814	1 AKH_BUCA1	08k9a9 buchnera ap	
24	84.5	11.7	575	1 RPOC_PLAFA	P21422 plasmidium	
25	84.5	11.7	609	1 YSW1_YEAST	P38280 saccharomyces	
26	84.5	11.7	1121	1 YJ09_YEAST	P47107 saecharomy	
27	84	11.6	861	1 SYL_BUCA1	Q8k9a9 buchnera ap	
28	83.5	11.5	368	1 TRMU_BUCA1	P57349 helicobacte	
29	83.5	11.5	378	1 PYRX_HELPJ	Q9zma9 thermomaer	
30	83.5	11.5	481	1 SYEL_THETN	P57505 buchnera ap	
31	83	11.5	212	1 DSBA_BUCA1	051737 borrelia bu	
32	83	11.5	862	1 MUTS_BORBI	P21358 candida gla	
33	82.5	11.4	339	1 RMAR_CANGA		

FT	DOMAIN	600	1014	COILED COIL (POTENTIAL).
SQ	SEQUENCE	1044	AA:	119127 MW: 5240E0174725A59 CRC64;
Qy	Query Match	13.63	Score	98.5; DB 1; Length 1044;
DB	Best Local Similarity	27.98	Pred. No.	2.1;
DB	Matches	39;	Indels	31; Gaps 8;
Qy	22 IHLEKVKONGSPNYDVKITFIDGYL---YIKNSKGVLKDLYKNVISVALK-RDY 75			
DB	673 IELDTYSNCKQMEEEQV-LKEGHESEIKDFLEHSKLTKQLDDDKNQFGISSLKNRDL 731			
Qy	76 LSLSLSNKRNKQIKFKN-----KHKHLENKFNYYVINEDIEKTRT----KNGLE 121			
DB	732 LS-----ELEVKSLANSLALESNNKKLENDLNL-LTEKLNNKNADESFKNTI-R 781			
Qy	76 EVILNKMLLSILGNEENLL 141			
DB	782 EAELSKRALNDNEGKNNII 801 ↗			
RESULT 2				
YAF3_SCHPO	ID YAF3_SCHPO STANDARD;	PRT;	1044 AA.	
AC	009857; Q9P7V0;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypothetical protein C29E6_03C in chromosome 1.			
GN	SPAC29E6_03C OR SPAC30_07C.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Euksaryota: Fungi: Ascomycota: Schizosaccharomycetes;			
OC	Schizosaccharomyces; Schizosaccharomycetidae;			
OX	NCBI_TaxID=4896;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN# 972;			
RC	LINE# 21848401; PubMed=11859360;			
RA	Wood V., William R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,			
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,			
RA	Holroyd S., Hornsby T., Howarth S., Huchle E.J., Hunt S., Jageis K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Volckaert G., Aert R., Robben J., Grimonprez B.,			
RA	Weltjens I., Vanstreels E., Reiger M., Schaefer M., Mueller Auer S.,			
RA	Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,			
RA	Gofeau A., Cadieu F., Dreano S., Glocu S., Lelaire V., Motter S.,			
RA	Galibert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Lucas M., Rochet M., Gaillard C., Talada V.A., Garzon A., Rhode G.,			
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,			
RA	Cerruti L., Lowe B., McCombie W.R., Paulsen I., Potashkin J.,			
RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,			
RA	"The genome sequence of Schizosaccharomyces pombe."			
RL	NATURE 411:871-880(2002).			
CC	-!- SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: Z66325; CAA91125.1; ALT-SEQ.			
DR	EMBL: AL16538; CAB6466.1; -			
DR	PIR: T50213; T50213			
DR	GeneDB_Spome: SPAC9E6_03C; -			
DR	InterPro: IPR006953; Usol_P115_head_1			
DR	PFAM: PF04869; Usol_P115_head_1			
CC	Hypothetical protein_c01_colled_c01.			
CC	KW			

DR modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC

DR EMBL; AF210133; AAA26940.2; -;
 DR EMBL; AE014955; AAN58874.1; -;
 DR PIR; A44798; A44798.
 KW Transcription regulation; Complete proteome.

FT CONFLICT 361 363 KEP -> RES (IN REF. 1).
 FT CONFLICT 441 441 V -> A (IN REF. 1).
 FT CONFLICT 447 447 M -> I (IN REF. 1).
 FT CONFLICT 482 482 K -> R (IN REF. 1).
 FT CONFLICT 539 539 C -> R (IN REF. 1 AND 3).
 FT CONFLICT 551 551 H -> R (IN REF. 1 AND 3).
 FT CONFLICT 620 620 L -> P (IN REF. 1 AND 3).
 SQ SEQUENCE 650 AA; 75337 MW; 02F122435B7C97A CRC64;

Query Match 13.2%; Score 95.5; DB 1; Length 650;
 Best Local Similarity 25.8%; Pred. No. 2.2; Gaps 9;
 Matches 42; Conservative 30; Mismatches 44; Indels 47; Gaps 9;

QY 1 MELQAFVFFEDENLSSSSGSIILEVKVONCSPNYDFKTFIDGYLYIKNKSGVILDKY 60
 DB 29 LKVSRVTVRTISDOLNTINSIILKEN-QNY-----FLVG----- 65

QY 61 DLKVNVISVALK - RDYLSLSSLSSNKKQIKRFKNKTKNKKNFNLVYN-----EDIKRR 113
 DB 66 ELANLASLISLDTYEQYERUNLTYKLMSLSSSTNEQLOEEFVNSVNTIIQDIAEIKR 125

QY 114 IT-----KNGLEEVTLNK----MILSILLGNEENILQIS 144
 DB 126 LADFDLRLDKKGY - RLGVNKNTLRLRAILITNN---LISIS 163

RESULT 4
 ID ALR_RICPR PRIM_MYCPU STANDARD PRT; 404 AA.
 AC Q92525;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alanine racemase (EC 5.1.1.1).
 GN ALR OR RP095.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 Rickettsiaceae; Rickettsiae; Rickettsia.
 NCBI_TAXID=782;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S. G. E., Zomorodipour A., Andersson J. O.,
 Sicheritz-Ponten T., Alsmark U. C. M., Podowski R. M., Naeislund A. K.,
 Eriksson A.-S., Winkler H. H., Kurland C. G.
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 mitochondrial DNA."
 RL Nature 396:133-140(1998),
 RN [2]
 RP DOMAIN RPEI.
 RX MEDLINE=20485642; PubMed=1101030655;
 RA Ogata H., Audic S., Barbe V., Artiguenave F., Fournier P.-E.,
 RA Raoult D., Claverie J.-M.;
 RT "Selfish DNA in protein-coding genes of Rickettsia.";
 RL Science 290:347-350(2000).
 CC -!- FUNCTION: Provides the D-alanine required for cell wall
 biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
 step.
 CC -!- SIMILARITY: Belongs to the alanine racemase family.
 CC -!- SIMILARITY: Contains 1 RPEI insert domain.

RESULT 5
 PRIM_MYCPU STANDARD PRT; 602 AA.
 ID PRIM_MYCPU
 AC Q98QD3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA primase (EC 2.7.7.-).
 GN DNAG OR MYPU_4530.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
 NCBI_TAXID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dydwig K., Wroblewski H., Viari A., Rocha E. P. C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 Mycoplasma pneumoniae.";
 RL Nucleic Acids Res. 29:2145-2153(2001).
 CC -!- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL
 RNA PRIMERS FOR THE OKAZAKI FRAGMENTS ON BOTH TEMPLATE STRANDS AT
 CC REPLICATION FORKS DURING CHROMOSOMAL DNA SYNTHESIS.
 CC -!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (BY SIMILARITY).
 CC -!- SUBUNIT: Monomer (By similarity).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC used by non-profit institutions.

modified and this statement is not removed. Usage by and for commercial purposes requires a license agreement. (See <http://www.isb-sib.ch/announce/>) or send an email to license@isb-sib.ch

or send an email to license@isb-sib.ch

RESULT 7						
YPJH_BACSU						
ID	YPJH_BACSU	STANDARD:	PRT:	377 AA.		
AC	PA2982;					
DT	01-NOV-1995	(Rel. 32)				
RX	MEDLINE#96349105;					
RA	Sorokin A.V.,	Zumstein E.,	Galleron N.,	Ehrlich S.D.,		
RA	Azevedo V.,					
RA	Serrur P.,					
RT	"Sequence analysis of the <i>Bacillus subtilis</i> chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome.";					
RL	Microbiology 142:2005-2016(1996).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=168 / Marburg;					
RX	MEDLINE#98044033; PubMed=9384377;					
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,					
RA	Bertero M.G., Bessieres P., Bolotin A., Borchart S.,					
RA	Bourriau R., Bourriau L., Brans A., Braun M., Brignell S.C., Bron S.,					
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,					
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,					
RA	Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,					
RA	Entian K.D., Errington J., Fabret C., Ferrari E., Fouger D.,					
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,					
RA	Ghini S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,					
RA	Guiseppi G., Guy P.J., Haga K., Haines J., Harwood C.R., Heraut A.,					
RA	Hilbert H., Hollsbepp S., Hosono S., Hulio M.P., Itaya M., Jones L.,					
RA	Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,					
RA	Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kunano M.,					
RA	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,					
RA	Lee S.M., Levine A., Liu H., Masuda S., Muel C., Medigue C.,					
RA	Medina N., Mellado M., Miura M., Moretti D., Nakai S., Noback M.,					
RA	Nozono D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,					

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Puic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaike Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scuffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.-S., Takeuchi M., Tacconi E., Takahashi H., Takemaru K., Tanaka T., Terpstra P., Tognoni A., Tomatsu V., Uchiyama S., Vandembol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedder E., Weitzenegger T., Winters P., Wipat A., Yamamoto K., Yamane K., Yata K., Yoshida K., Yoshioka H.F., Zumstein E., Yoshikawa H., Danchin A.; subtilis*;	CC -!- FUNCTION: REGULATES THE EXPRESSION OF GLUCOSYLTRANSFERASE (GTfG). CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
RT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RL Nature 390:249-256(1997).	CC -!- The complete genome sequence of the Gram-positive bacterium Bacillus subtilis*;
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.	CC -!- The complete genome sequence of the Gram-positive bacterium Bacillus subtilis*;
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -!- The complete genome sequence of the Gram-positive bacterium Bacillus subtilis*;	CC -!- The complete genome sequence of the Gram-positive bacterium Bacillus subtilis*;
DR EMBL; L38424; AAA92877.1; ALT_SEQ.	DR EMBL; L38424; AAA92877.1; ALT_SEQ.
DR EMBL; AAB38445.1;	DR EMBL; AAB38445.1;
DR EMBL; Z99115; CAB14162.1;	DR EMBL; Z99115; CAB14162.1;
DR PIR; G69937; G69937.	DR PIR; G69937; G69937.
DR Subtilist; BG11213; YPJH.	DR Subtilist; BG11213; YPJH.
DR InterPro; IPR001296; Glyco_trans_1.	DR InterPro; IPR001296; Glyco_trans_1.
DR Pfam; PF00534; Glycos_transf_1.	DR Pfam; PF00534; Glycos_transf_1.
KW Hypothetical protein; Transferase; Glycosyltransferase;	KW Hypothetical protein; Transferase; Glycosyltransferase;
KW Complete proteome.	KW Complete proteome.
SEQUENCE 377 AA; 41978 MW; 2DB1AB344D6536AA CRC64;	SEQUENCE 377 AA; 41978 MW; 2DB1AB344D6536AA CRC64;
Query Match 12.6%; Score 91; DB 1; Length 377;	Query Match 12.6%; Score 91; DB 1; Length 377;
Best Local Similarity 23.0%; Pred. No. 2.8;	Best Local Similarity 23.0%; Pred. No. 2.8;
Matches 37; Conservative 31; Mismatches 43; Indels 50; Gaps 8;	Matches 37; Conservative 31; Mismatches 43; Indels 50; Gaps 8;
Qy 7 FVFFEDMNLSSSSGSIILEVKVQNCNSNNYDFK-----ITFIDGYLYIKNKSGVILD 58	Qy 7 FVFFEDMNLSSSSGSIILEVKVQNCNSNNYDFK-----ITFIDGYLYIKNKSGVILD 58
Db 140 FATESSRVTAVSALLAE-----TYDLIKPKEKKIETIYNFDERVYKKNTAAIKE 191	Db 140 FATESSRVTAVSALLAE-----TYDLIKPKEKKIETIYNFDERVYKKNTAAIKE 191
Qy 59 KYDLKVNISVLVALDKYLSLSLNKQIKR-----FKNIKHNLRKFLNKFNYVNDIE 111	Qy 59 KYDLKVNISVLVALDKYLSLSLNKQIKR-----FKNIKHNLRKFLNKFNYVNDIE 111
Db 192 KUGI-----LPDEVKVIVHSNFRVKVQDVIRYFRNTAG--KTKAKLULLGGPE 240	Db 192 KUGI-----LPDEVKVIVHSNFRVKVQDVIRYFRNTAG--KTKAKLULLGGPE 240
Qy 112 KR-----ITKNGTLEEVILNKMLLSILIGNE---ENLIQIS 144	Qy 112 KR-----ITKNGTLEEVILNKMLLSILIGNE---ENLIQIS 144
Db 241 KSTACEELRKYLEDQV-----LMGLGNQRVEDLYSIS 273	Db 241 KSTACEELRKYLEDQV-----LMGLGNQRVEDLYSIS 273
RESULT 8	RESULT 8
RGCG_STRGCG STANDARD; PRT; 297 AA.	RGCG_STRGCG STANDARD; PRT; 297 AA.
ID RGCG_STRGCG	ID RGCG_STRGCG
AC P4_330;	AC P4_330;
DT 01-FEB-1996 (Rel. 33, Created)	DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein in rgg.	DE Protein in rgg.
GN RGG.	GN RGG.
OS Streptococcus gordoni Challis.	OS Streptococcus gordoni Challis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.	OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
OX NCBI_TaxID=29390;	OX NCBI_TaxID=29390;
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.
RX MEDLINE=92276337; PubMed=1534326;	RX MEDLINE=92276337; PubMed=1534326;
RA Sulavik M.C., Tardif G., Clewell D.B.;	RA Sulavik M.C., Tardif G., Clewell D.B.;
RT "Identification of a gene, rgg, which regulates expression of	RT "Identification of a gene, rgg, which regulates expression of
RT glucosyltransferase and influences the spp phenotype of Streptococcus	RT glucosyltransferase and influences the spp phenotype of Streptococcus
RT gordoni Challis.";	RT gordoni Challis.";
RL J. Bacteriol. 174:3577-3586(1992).	RL J. Bacteriol. 174:3577-3586(1992).

or send an email to license@isb-sib.ch).

CC or send an email to license@isb-sib.ch).

CC CC

DR DR EMBL; AP004171; BAC44178.1; ..

DR DR HAMAP; MF_00049; ..

DR DR PF00133; tRNA-synt_1; 1.

DR DR TIGRFAMS; TIGR00396; leus_bat; 1.

DR DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.

DR KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

DR KW Complete proteome.

DR FT SITE 39 50 "HIGH" REGION.

DR FT SITE 575 579 "KMSKS" REGION.

DR FT BINDING 578 578 ATP (BY SIMILARITY).

DR SQ SEQUENCE 799 AA; 93.29 MW; 3B62E3CD7D06FE CRC64;

Query Match 12.4%; Score 89.5; DB 1; Length 799;

Best Local Similarity 26.1%; Pred. No. 8.1;

Matches 36; Conservative 21; Mismatches 42; Indels 39; Gaps 5;

Qy 7 FVFFEDNLSSSSSIHLEVKQNCSPNVDYFK-----ITFDGYLYIKNK-- 52

Db 661 FMENDFDNLVISEMMIFINCEYKEVINYDMLNFCLSCFAPPITEINEFLKNKKF 720

Qy 53 -SGVILDKYDKLKNV-----ISVALKRDYLSLSLNQIQKFKFN 91

Db 721 ISDNLWPKYDEKKIVETTIKPYQINGKIREVLEINLQATQDVDAIKNEKLKWN 780

RESULT 11

OBP_BOVIN STANDARD; PRT; 159 AA.

AC OBP_BOVIN ID: P07435; STANDARD; PRT; 159 AA.

DT 01-APR-1988 (Rel. 07, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Odorant-binding protein (OBP) (Olfactory mucosa pyrazine-binding protein).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos.

NCBI_TaxID:9913; RN [1]

RP SEQUENCE [1]

RA MEDLINE:90076175; PubMed=2512125;

RA Tirindelli R., Keen J.N., Cavaggioni A., Eliopoulos E.E., Findlay J.B.C.; RA "Complete amino acid sequence of pyrazine-binding protein from cow nasal mucosa." FEBS Lett. 212:225-228(1987).

RA RN [3]

RP X-RAY CRYSTALLOGRAPHY. RX MEDLINE:92322903; PubMed=1623143;

RA RA Monaco H.L., Zanotti G.; RT "Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence similarity." Biopolymers 32:457-465(1992).

RA RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). RX MEDLINE:97057532; PubMed=8501871;

RA RA Blanchet M.A., Bains G., Pelosi P., Pevsner J., Snyder S.H., Monaco H.L., Amzel L.M.;

SYL_MYCPE STANDARD; PRT; 799 AA.

ID SYL_MYCPE ID: Q8EP18; PRT; 799 AA.

AC AC DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DE DE Leucyl-tRNA Synthetase (EC 6.1.1.4) (Leucine-tRNA ligase) (LeuRS).

GN GN OS MYPSE890. Mycoplasma penetrans. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OC OC NCBI_TaxID=28327; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HP-2; RX MEDLINE:87134269; PubMed=3817156;

RA RA Sasaki Y., Isikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; RT "The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans." Nucleic Acids Res. 30:5293-5300(2002).

RL RL "- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA (Leu) = AMP + diphosphate + L-leucyl-tRNA (Leu)."

CC CC "- SUBCELLULAR LOCATION: Cytoplasmic.

CC CC "- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

RT "The three-dimensional structure of bovine odorant binding protein and its mechanism of odor recognition.";
 RT Nat. Struct. Biol. 3:934-939(1996).
 RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=956433075; PubMed=8836103;
 RA Tegoni M., Ramoni R., Bignetti E., Spinelli S., Cambillau C.;
 RT "Domain swapping creates a third putative combining site in bovine odorant binding protein dimer.";
 RL Nat. Struct. Biol. 3:863-867(1996).

CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Belongs to the lipocalin family.
 DR PIR: PS06843; S0843.
 DR PDB: 1PBO; 23-JUL-97.
 DR PDB: 1OBP; 14-OCT-96.
 DR PDB: 1G85; 26-JUN-02.
 DR PDB: 1HN2; 05-DEC-01.
 DR InterPro: IPR00566; Lipocalin_CytFABP.
 DR Pfam: PF00661; Lipocalin; 1.
 DR PROSITE: PS0021; LIPOCALIN; 1.
 KW Olfaction; transport; Lipocalin; 3D-structure.

FT HELIX 11 13
 FT STRAND 39 46
 FT TURN 47 50
 FT STRAND 51 60
 FT TURN 61 62
 FT STRAND 63 73
 FT TURN 75 76
 FT STRAND 79 82
 FT STRAND 86 94
 FT STRAND 98 106
 FT TURN 108 109
 FT STRAND 112 121
 FT HELIX 126 138
 FT TURN 139 140
 FT HELIX 143 145
 FT STRAND 146 148
 SQ SEQUENCE 159 AA;
 MW: 33858BBF1D03D4A8 CRC64;
 RESULT 13
 ALR_RICCN STANDARD; PRT; 355 AA.
 ID ALR_RICCN
 AC AC
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Alanine racemase (EC 5.1.1.1).
 GN ALR OR RC0138.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; Alpha-proteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RL STRAIN=Raillish 7;
 RX MEDLINE=2142074; PubMed=11557833;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
 RL Science 293:2093-2098 (2001).
 CC -!- FUNCTION: Provides the D-alanine required for cell wall biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first step.
 CC -!- SIMILARITY: Belongs to the alanine racemase family.
 CC

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21;
 RA Sekito T., Okamoto K., Kitano H., Yoshida K.;
 RT "Yeast Hansenula wingei mitochondrial genome's complete DNA sequence demonstrated unique characteristics.";
 RL Nucleic Acids Symp. Ser. 31:233-234 (1994).
 CC -!- FUNCTION: ESSENTIAL FOR MITOCHONDRIAL PROTEIN SYNTHESIS AND REQUIRED FOR THE MATURATION OF SMALL RIBOSOMAL SUBUNITS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE VARI FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL: D31785; BAA06578; 2/-.
 DR PTRR: S58755; S58755.
 DR Pfam: PF05316; Yeast_VARI; 1.
 KW Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 386 AA; 44904 MW; 9AD0D625F303E88F CRC64;
 Query Match 12.1%; Score 87.5; DB 1; Length 386;
 Best Local Similarity 33.3%; Pred. No. 5.4;
 Matches 20; Mismatches 39; Indels 19; Gaps 7;
 Qy 39 KTFIDGYLYTKNSGV---ILDKYDLKVNISVALDKRDYLSSLSLNKKQIK-----87
 Db 44 KINSWDQLYKKNNKVINTWLDRYSLKLKIFKVRVNINNNINGQIKDIYINKP 103
 Qy 88 KFPKNIKHLKRNFKNLYVINYNEDEKTRKNGKLEEVTLNKMMSLILLGNEENLQLIS 144
 Db 104 KPKHTINKVYIN-FN-YLSSN---NFTINDI-DNNNNKYYTSI-INDINNLIGS 152
 RESULT 14
 ALR_RICCN STANDARD; PRT; 355 AA.
 ID ALR_RICCN
 AC AC
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Alanine racemase (EC 5.1.1.1).
 GN ALR OR RC0138.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; Alpha-proteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RL STRAIN=Raillish 7;
 RX MEDLINE=2142074; PubMed=11557833;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
 RL Science 293:2093-2098 (2001).
 CC -!- FUNCTION: Provides the D-alanine required for cell wall biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first step.
 CC -!- SIMILARITY: Belongs to the alanine racemase family.
 CC

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AE008579; AAI026666.1; - .
 DR PIR; H9715; H9715.
 DR HAMAP; MF_01201; - .
 DR InterPro; IPR000821; Ala_racemase.
 DR Pfam; PF0168; Ala_racemase_c; 1.
 DR Pfam; PF0168; Ala_racemase_N; 1.
 PRINTS; PRO0992; ALARACEMASE.
 DR TIGRFAMS; TIGR0492; alr; 1.
 DR PROSTRES; PS00395; ALANINE_RACEMASE; 1.
 KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
 KW Complete proteome. ACT_SITE 34 CATALYTIC BASE SPECIFIC TO D-ALANINE
 FT ACT_SITE 249 249 (BY SIMILARITY). CATALYTIC BASE SPECIFIC TO L-ALANINE
 FT BINDING 34 34 (BY SIMILARITY). PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE: 355 AA; 39488 MW; 63M489ED384081EB CRC64;
 FT ACT_SITE 34 CATALYTIC BASE SPECIFIC TO D-ALANINE
 FT ACT_SITE 249 249 (BY SIMILARITY). CATALYTIC BASE SPECIFIC TO L-ALANINE
 FT BINDING 34 34 (BY SIMILARITY). PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 Query Match 12.0%; Score 87; DB 1; Length 355;
 Best Local Similarity 24.5%; pred. No. 5.4;
 Matches 35; Conservative 37; Mismatches 49; Indels 22; Gaps 7;
 Qy 20 GSIHDEK--VKQNCSPNYDFKTFIDGYIYIKNSVILDKYDKNVISVALKDYL 77
 Db 41 GAVQSKALLEENCR---HFFVASSEEVNLRLAQLGDVNLYVNGFEHDALEIEN 96
 Qy 7B LS--LSNNKOK---KKFKNKNK---HLLKNKNF-N-LVYINEDJEKRITKGTL-E--- 121
 Db 97 LTPVNLNLQRQLEIWKFSNLKNRLPCYLHFNTGINRLGLSSDEEQLNDRDLJKGLDL 156
 Qy 122 EVILKMLIISLLGNEENLQIS 144
 Db 157 QYIISHLATEEIDNPYNLEQLN 179
 RESULT 14
 RPOC_ASTLO STANDARD PRT; 575 AA.
 AC P58713;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6).
 GN RPOC1.
 OS Astasia longa (Euglenophycean algae).
 OC Euglenozoa; Euglenida; Euglenales; Euglena.
 OX NCBI_TAXID=3037;
 RN SEQUENCE FROM N.A.
 RC STRAIN=CCAP 1204-17a;
 RX MEDLINE=2108022; PubMed=11212895;
 RA Goetel, G., Hachtel, W.;
 RT "Complete gene map of the plastid genome of the nonphotosynthetic euglenoid flagellate *Astasia longa*." ;
 RL Protist 151:307-351(2000).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF RNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N nucleotide triphosphate = N diphosphate + (RNA)(N).
 CC -!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta'.
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

CC
 DR EMBSP; Q9KQWU6; 1HOM.
 DR InterPro; IPR00722; RNA_pol_A.
 DR InterPro; IPR007080; RNA_pol_Bpb1_1.
 DR InterPro; IPR006592; RNA_pol_A_N.
 DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
 DR Pfam; PF0623; RNA.pol.Rpb1_2; 1.
 SMART; SM00663; RPOLA_N; 1.
 KW Transferase; Transcription; DNA-dependent RNA polymerase; Chloroplast.
 SO SEQUENCE 575 AA; 67075 MW; C83269D0B54F8DAF CRC64;
 CC
 DR A294735; CAAC24618.1; - .
 DR HSSP; Q9KQWU6; 1HOM.
 DR InterPro; IPR00722; RNA_pol_A.
 DR InterPro; IPR007080; RNA_pol_Bpb1_1.
 DR InterPro; IPR006592; RNA_pol_A_N.
 DR Pfam; PF04997; RNA.pol.Rpb1_1; 1.
 DR Pfam; PF0623; RNA.pol.Rpb1_2; 1.
 SMART; SM00663; RPOLA_N; 1.
 KW Transferase; Transcription; DNA-dependent RNA polymerase; Chloroplast.
 CC
 DR Query Match 12.0%; Score 87; DB 1; Length 575;
 DR Best Local Similarity 26.7%; pred. No. 9;
 DR Matches 46; Conservative 24; Mismatches 54; Indels 48; Gaps 9;
 DR Qy 13 ENLSSSSGSIHLERVKONGSPNYDFKTFIDGYIYIKNSVILDKYDKNVISVALK 72
 DR 161 EAINDILSKIDLETKLKLINTHQQK---ERNKNIKHNKHKNKFL---KFKNIKHNKHKNKFL--- 215
 DR 73 RDYL-----SLSLSNNKQIK----SLSLSNNKQIK----SLSLSNNKQIK----SLSLSNNKQIK---- 216
 DR 216 FSWLLFKYLPLVLPNVRPTIMKMKNQOQSNDLNTLYASINTVNNKTKLESLJPDNYFI 275
 DR Qy 107 NEDI-EKRIT-----KNGILEEVLNKMLLSI---LLOGNE---ENL 141
 DR 276 NEKILLQKKVQDQLINNEKYKENKLKTSITENIKGREGIIKENML 327
 DR
 RESULT 15
 RPOP_NEUIN RPOP_NEUIN STANDARD PRT; 811 AA.
 AC P33541;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable DNA-directed RNA polymerase (EC 2.7.7.6).
 OX Mitochondrion.
 OG Plasmid kallio.
 OC Eukaryota; Fungi; Ascomycota; Pezizomyctina; Sordariomycetes;
 OC Sordariomycetidae; Sordariaceae; Neurospora.
 OX Neurospora intermedia.
 OG
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92035090; PubMed=1914129;
 RA Chan, B.S.-S., Court, D.A., Vierula, P.J., Bertrand, H.;
 RA "The kallio linear senescence-inducing plasmid of Neurospora is an invertron and encodes DNA and RNA polymerases." ;
 RN [1]
 RN Curr. Genet. 20:245-237(1991).
 RN [2]
 RP SEQUENCE OF 1-58 FROM N.A.
 RX MEDLINE=93024309; PubMed=1406582;
 RA Vierula, P.J., Bertrand, H.;
 RT "A deletion derivative of the kallio senescence plasmid forms hairpin and duplex DNA structures in the mitochondria of Neurospora." ;
 RT Mol. Gen. Genet. 234:361-368(1992),
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).
 CC -!- SIMILARITY: BELONGS TO THE PHAGE AND MITOCHONDRIAL RNA POLYMERASES FAMILY.
 CC -!- FAMILY.
 CC

This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC	EMBL; X52106; CAA36326_1;
DR	PIR; S17908; S17908.
DR	HSSP; P00573; 1ARO.
DR	InterPro; IPR002092; RNA_pol_phage.
DR	Pfam; PF00940; RNA_Pol; 1.
DR	PS00489; RNA_POL_PHAGE_2;
DR	PROSITE; PS00489; RNA_POL_PHAGE_2;
DR	PS00590; RNA_POL_PHAGE_1;
KW	Transfere; Transcription; DNA-directed RNA polymerase;
KW	Mitochondrion; Plasmid.
FT	ACT_SITE 470 BY SIMILARITY.
FT	ACT_SITE 540 BY SIMILARITY.
FT	ACT_SITE 718 BY SIMILARITY.
SQ	SEQUENCE 811 AA; 94800 MW; 286225A36B625BBC CRC64;

Query Match 12.0%; Score 87; DB 1; Length 811;
 Best Local Similarity 22.8%; Pred. No. 13;
 Matches 34; Conservative 40; Mismatches 45; Indels 30; Gaps 9;

Qy	3 LKQAFVFFEDENLSSSSGSIHLKVKQNCSPNQDFKTFIDGYLY-IKNKSGVYLDKYD 61
Db	4 31 MDKEFTIKAESPTLPAAFCUMLRKIEN--PDYPVNPIFLDATSGVQIFAAMLID-LE 487
Qy	62 LKNVISLV ---ALKRDYLSSLNSNNQI ---KKFKNIK ---NKHLKNK --- 100
Db	488 LGKVNLINSGESVNDYFSQQLPALNKATNEAEKKFKNLKFSDISLNRSLLKKVMTKS 547
Qy	101 FNL---VIVINEDIEKRITKNGLLEEVLINK 127
Db	548 YNTTYGITEQQLSKLEK ---VEKIVISK 573

Search completed: July 24, 2003, 20:06:34
 Job time : 27.2468 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using SW model
 Run on: July 24, 2003, 20:01:59 ; Search time 109,403 Seconds
 (Without alignments)
 Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5
 Title: US-09-546-136-5
 Perfect score: 723
 Sequence: 1 MELKQAFVFEEDENLSSSG.....LNKMLLSILLGNEENNLQIS 144
 Searched: 830525 seqs., 258052604 residues
 Total number of hits satisfying chosen parameters: 830525
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

ALIGNMENTS							
RESULT 1		PRELIMINARY;		PRT:		144 AA.	
OS	052975	ID	052975;	SEQUENCE FROM N.A.			
AC	052975;	STRAIN-TYPE	E Iwana;				
DT	01-JUN-1998	RX	MEDLINE=9465394;				
DT	01-JUN-1998	RA	PubMed=9465394;				
DT	01-JUN-1998	RA	Robot T., Yonekura N., Hariya Y., Isogai E., Amano K.,				
DT	01-NOV-1998	RA	Fujii N.				
DE	ORF-XI.	RT	"Gene arrangement in the upstream region of Clostridium botulinum type E and Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types."				
OC	Clostridium botulinum.	RT	EFMS Microbiol. Lett. 158:215-221(1998).				
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;	RL	EMBL; D88418; BAA24800.1.				
OX	Clostridium.	DR	3A4F7DB7F67670BC CRG64;				
RN	NCBI_TaxID=1491;	SQ	SEQUENCE 144 AA; 16767 MW;				
Query Match							
Qy	1	Best Local Similarity	100.0%	Score	723;	DB	2;
Qy	1	Matches	144	Length	144;		
Db	1	Conservative	100.0%	Pred. No.	5.7e-45;		
Qy	1	MELKQAFVPEFDENLSSSSGSLHLREVKQNCSPNYDFKIPITDGYLYIKNSGVILDKY	1	Mismatches	0;	Indels	0;
Db	1	MELKQAFVPEFDENLSSSSGSLHLREVKQNCSPNYDFKIPITDGYLYIKNSGVILDKY	1	Gaps			
Qy	61	DILKNVISLVALDKRDYLSSLSSNKQIKKFKNIKNHKLKNKENLYVINEDIKRITKGIL	1				
Db	61	DILKNVISLVALDKRDYLSSLSSNKQIKKFKNIKNHKLKNENLYVINEDIKRITKGIL	1				
Qy	121	EVEILNKMLLSLLGNENFLGQS	144				

ALIGNMENTS							
RESULT 1		PRT:		AA.			
OS	052975	PRELIMINARY;	PRT:	144	AA.		
ID	052975;						
AC	OS2975;						
DT	01-JUN-1998	(TREMBLrel. 06, Created)					
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)					
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)					
DE	ORF-XI.						
OC	Bacteria; Clostridium; Clostridia; Clostridiales; Clostridiaceae; Clostridium.						
OC	NCBI_TaxID:1491;						
OX	NCBI_TaxID:1491;						
RN	111]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN-TYPE E Iwana;						
RX	MEDLINE=98126542; PubMed=9465394;						
RA	Rubota T., Yonekura N., Hariya Y., Isogai H., Amano K., Fujii N.						
RA	"Gene arrangement in the upstream region of Clostridium botulinum type E and Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types.";						
RT	EFMS Microbiol. Lett. 158:215-221(1998).						
RL	EMBL; D88418; BAA24880.1;						
DR	SEQUENCE 144 AA; 16767 MW;						
SQ	3A4F7DB7E67670BC CRC64;						
Query Match	100.0%	Score 723;	DB 2;	Length 144;			
Best Local Similarity	100.0%	Pred. No. 5	7e-45;				
Matches	144	Conservative: 0;	Mismatches 0;	Indels 0;	Gaps		
Qy	1 MELKQAVFPEFDENLSSSGS1HLEVKQNSCPNQDYFKTFIDGYLYIKNSGVLDKY	6					
Db	1 MELKQAVFPEFDENLSSSGS1HLEVKQNSCPNQDYFKTFIDGYLYIKNSGVLDKY	6					
Qy	61 DIKRNVISVALKDYLSSLSSNQKIKFKNNKNKHLKNKFNFYVINEDIEKRITKGIL	1					
Db	61 DIKRNVISVALKDYLSSLSSNQKIKFKNNKNKHLKNKFNFYVINEDIEKRITKGIL	1					
Qy	121 EEVILNKMLLSLLGNEENLICIS 144						

Result No.	Query				Description
	Score	Match Length	DB	ID	
1	723	100.0	144	2	052975 clostridi
2	553	76.5	142	2	050600 clostridi
3	540	74.7	142	2	050597 clostridi
4	111.0	15.4	2279	5	081JPF6 plasmodiu
5	110.5	15.3	1782	5	Q812L1 plasmodiu
6	106	14.7	796	5	081EN5 plasmodiu
7	105.5	14.6	607	5	081CC9 plasmodiu
8	105.5	14.6	1213	5	Q81C20 plasmodiu
9	105.5	14.6	2961	5	Q815T5 plasmodiu
10	104.5	14.5	1001	16	025314 helicoba
11	104.5	14.5	1226	5	Q81L77 plasmodiu
12	104	14.4	245	17	08TJRO methanosa
13	102.5	14.2	227	5	Q81CK6 plasmodiu
14	102	14.2	4202	5	Q812S8 plasmodiu
15	101	14.0	651	5	09av6 quillard
16	99	13.7	1284	5	08av6 quillard

Qy	4	RQAFV-FEFDEN-----LSSSSSIHLEVKVQNCSPNYDFKTFIDGYLYIKNSGVY 56	OC	Helicobacteraceae; Helicobacter.
Db	63	KENPFVSFKDKNNNLTISVKSTKLKSLIFDKKKNNLKK----KVTKDGYIRKND-EIY 116	NCBI_TaxID=10;	
Oy	57	LDKYDLKNVNTSLVALRK---DYNLSL---SNMKQIKK---FKNIKNKRHLNKNFNLVYI 106	RN	
Db	117	LDKNNFLNEINLLRKKLKINDYKLDDLFHKDSNISIQKPYVTFDDYKNVNIEKNSKEII 176	SEQUENCE FROM N.A. STRAIN=26655 / ATCC 700392; MEDLINE=97394467; PubMed=9252185;	
Qy	107	N-----EDIEKRTKNGLLEEV--ILNKMLLISLGNEENLIQIS 144	RA	Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Sutton C.M., Gill S., Doughtery B.A., Fleischmann R.D., Ketchum K.A., Klein H.-P., Peterson S., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson J., Loftus B., Richardson D., Dodson R., Khalak H.G., McKenney K., Fitzgerald L., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Watchey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
Db	177	NFLKNCLENKKYINTHSSVVELRGTFNDELNPILNETLQKIS 222	RT	The complete genome sequence of the gastric pathogen Helicobacter pylori.
Qy	9	Q815T5 PRELIMINARY; PRT: 2961 AA.	RL	Nature 388:539-547(1997).
ID	Q815T5	PRT: 2961 AA.	DR	TIGR; HP0592;
AC	Q815T5;		DR	InterPro; IPRO006935; ResIII.
DT	01-MAR-2003	(TREMBLrel 23, Created)	DR	PFam; PF04851; ResIII; 1.
DT	01-MAR-2003	(TREMBLrel 23, Last annotation update)	DR	Hypothetical protein; Complete proteome.
DE	Hypothetical protein.		SQ	SEQUENCE 1001 AA; 114809 MW; 1817F729A96F48B1 CRC64;
GN	PF0575W		Query Match	14.5%; Score 104.5; DB 16; Length 1001;
OS	Plasmodium falciparum (isolate 3D7).	Best Local Similarity 37.08%; Pred. No. 11;	Matches 34; Conservative 12; Mismatches 12;	Mismatches 12; Gaps 4;
OX	Plasmodium falciparum; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	DR	24 LEVKQNCSPNYDFKTF--IDGYLY--IKNKSGVILDKVLNVTSVALKRDYL 78	
RN	NCBI_TaxID=16329; 111	DR	118 LESTYKONIRITKDYLETFKRIKHTTYLEGVKSPSNII--NHYIKN-----QDBLSV 167	
RP	SEQUENCE FROM N.A.	DR	79 SLSNNKOIKKKNNKHNKHNKPNLVINEDI 110	
RC	STRAIN=3D7;	DR	168 LLTNSAIDKEGNLNKNSENLNFTKSFENI 199	
RX	MEDLINE=22255705; PubMed=12368864;	RESULT 11		
RA	Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Paulsen I.T., James K., Chan M.-S., Nene V., Salimov S.J., Suh B., Peterson J., Paulsen I.T., Craig A., Kyes S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Angiuoli S., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Vaidya A.B., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Catuccia D.J., Hoffman S.L., Ralph S.A., Fraser C.M., Barrell B.;	ID	Q81L77 PRELIMINARY; PRT: 1226 AA.	
RT	"Genome sequence of the human malaria parasite Plasmodium falciparum.";	AC	Q81L77;	
RL	Nature 414:498-511(2002)	DT	01-MAR-2003 (TREMBLrel 23, Created)	
DR	EMBL; AE014846; AAN36204; 1;	DT	01-MAR-2003 (TREMBLrel 23, Last sequence update)	
KW	Hypothetical protein.	DE	Hypothetical protein.	
SO	SEQUENCE 2961 AA; 350583 MW; 1A887A5BB5D0F69 CRC64;	GN	PF14_0371.	
Query Match	14.6%; Score 105.5; DB 5; Length 2961;	OS	Plasmodium falciparum (isolate 3D7).	
Best Local Similarity 25.0%; pred. No. 26;	Mismatches 29; Mismatches 54; Indels 49; Gaps 8;	OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
Matches 44;	Conservative 29; Mismatches 54; Indels 49; Gaps 8;	OX	NCBI_TaxID=36329;	
Qy	7 FVFEDEDNLSSGGSIHLEVKYKON---CSPNYD---YFKITFIDGY-----LYK 50	RN	SEQUENCE FROM N.A.	
Db	342 YVHDDEENQKYSSEPEKKCYKENICMENFEKSHNMKIQYVDFQKENTENGKILYK 401	RC	STRAIN=3D7;	
Qy	51 NKSGVILDKYDLK-----NVTSLVALKRDYLSLSNNKQIKKFKNKHNHLK 98	RX	MEDLINE=22255705; PubMed=12368864;	
Db	402 EKKG----NKYNNKEKMMCMNSHAEDDNMVQ---NNVLDNNMGNKKNKK-KMKKNNVK 454	RA	Gardner M.J., Hall N., Nelson K.E., Bowman S., Paulsen I.T., Bergeron J.A., Rutherford K., Salzberg S.L., Craig A., White O., Berriman M., Chai M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;	
Qy	99 NKFNIYVINYDIEDERITKNGLLE-----VILNKMLLSTLNGNEENL 140	RA	Carroll J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., Bergeron J.A., Hall N., Nelson K.E., Bowman S., Paulsen I.T., James K., Chai M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;	
Db	455 FMVDNYVINDVNSKMHNNHESLOENNYYSVLQIPNNNNRIRANVILNNFNL 510	RA	Genome sequence of the human malaria parasite Plasmodium falciparum.	
RESULT 10		RT	Genome sequence of the human malaria parasite Plasmodium falciparum.	
O25314	PRELIMINARY; PRT: 1001 AA.	RL	Nature 414:498-511(2002).	
ID	O25314	Created)	DR	AE014822; AAN36984; 1;
AC	O23314;	Last sequence update)	KW	Hypothetical protein.
DT	01-JAN-1998 (TREMBLrel 05,	SQ	SEQUENCE 1226 AA; 141666 MW; E3F53927DF73BE4 CRC64;	
DT	01-JAN-1998 (TREMBLrel 05, Last annotation update)	Best Local Similarity 22.28%; Pred. No. 13;	Query Match	14.5%; Score 104.5; DB 5; Length 1226;
DE	Type III restriction enzyme R protein (RPS).	Matches 42; Conservative 39; Mismatches 53; Indels 55; Gaps 8;	Best Local Similarity 22.28%; Pred. No. 13; Mismatches 53; Indels 55; Gaps 8;	
GN	HP0592.	OS	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;	
OC	Helicobacter pylori (Campylobacter pylori).			

search completed: July 24, 2003, 20:08:41
 Job time : 112.403 secs

Query Match	Best Local Similarity	Score	DB	Length
Matches 39; Conservative 26;	27.18;	Pred. No.	65;	4202;
Mismatches 51;	Indels 28;	Gaps 7;		
Qy 12 DENLSSSGS----THLEKVKONCSPNVDKFITFDGYIYIKNSGVV--LDKYDLK 63				
Db 30091 DENTOGDESSLNFLLTHLGSKYNSVNTYEIVKVNQKKYINNDTSILKKIQHDVFY 3060				
Qy 64 NWISLVALKRDYLSS-----NNKQIKKPKNIKRHL-MNKFNLVYVNDIE--KRI 114				
Db 3061 N----ICYKNEVITNNESYMMNNILERKKVYIRINKKHIDKKYYRGDKIGORKRL 3116				
Qy 115 TKNGILEEVILNKMLLSILLGNGEE 138				
Db 3117 ----KLYFSKPASSYVILKNE 3133				

RESULT 15

Q9AW16	PRELIMINARY;	PRT;	651 AA.
ID Q9AW16			
AC Q9AW16;			
DT 01-JUN-2001 (TREMBLrel. 17, Created)			
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE DNA primase.			
GN DNAG.			
OS Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.			
OX NCBI_TaxID=55529;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20087226; PubMed=10618395;			
RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,			
RA Cavalier-Smith T., Mayer U., Douglas S.;			
PT "Chloroplast protein and centrosomal genes, a tRNA intron, and odd			
PT telomeres in an unusually compact eukaryotic genome, the cryptomonad			
PT nucleomorph.";			
RT Proc. Natl. Acad. Sci. U.S.A. 97:200-205 (2000).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21223349; PubMed=11323671;			
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Dang L.,			
RA Wu X., Reith M., Cavalier-Smith T., Maier U.;			
PT "The highly reduced genome of an enslaved algal nucleus.";			
DR ENBM; AJ010592; CAC27055.1;			
DR HSSP; Q9X4D0; 1000			
DR InterPro; IPR006647; ToprIm_primate.			
DR InterPro; IPR006154; ToprIm_sub.			
DR InterPro; IPR002694; Znf_CHC2.			
DR Pfam; PF01807; zf-CHC2; 1.			
DR ProDom; PDD02276; ToprIm_primate; 1.			
DR ProDom; PDD02988; Znf_CHC2; 1.			
DR SMART; SM00493; ToprIM; 1.			
DR SQ SEQUENCE 651 AA; 77961 MW; 00F0FEB569058F3B CRC64;			

Query Match

Best Local Similarity	Score	DB	Length	
Matches 50; Conservative 27;	28.98;	Pred. No.	13;	651;
Mismatches 56;	Indels 40;	Gaps 11;		
Qy 2 ELKQAFYFFEDENLSSSSGI----HLEKVKQ--NCSPNVDYFKTFIDGYIYIKNSKG 54				
Db 167 ETIFYMLYKF-RNLSNLTMKLNLYGSNKKISQIINQENHEYRL---LKTKTMKY 219				
Qy 55 VILDKYDLKVNVI-----SLVALKRDYLSSLSL-----NRQIQKRFKNIK-NKHJUKNKF 101				
Db 220 VVVDKINKKVYRDFINERLVIPIRNIYCLTGFGARTINSKIPKYLNSENKFKKKK 279				
Qy 102 NYVINEDIEKRITK-----NGILEEVIL--NKMILS-LGNEENLQLI 143				
Db 280 ILF-SEEKSNISLKSCKCLICEGYLDSTIUFONGTRFASLGGSNNNQI 330				

results of **BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1059158413-09039-19779

Query=

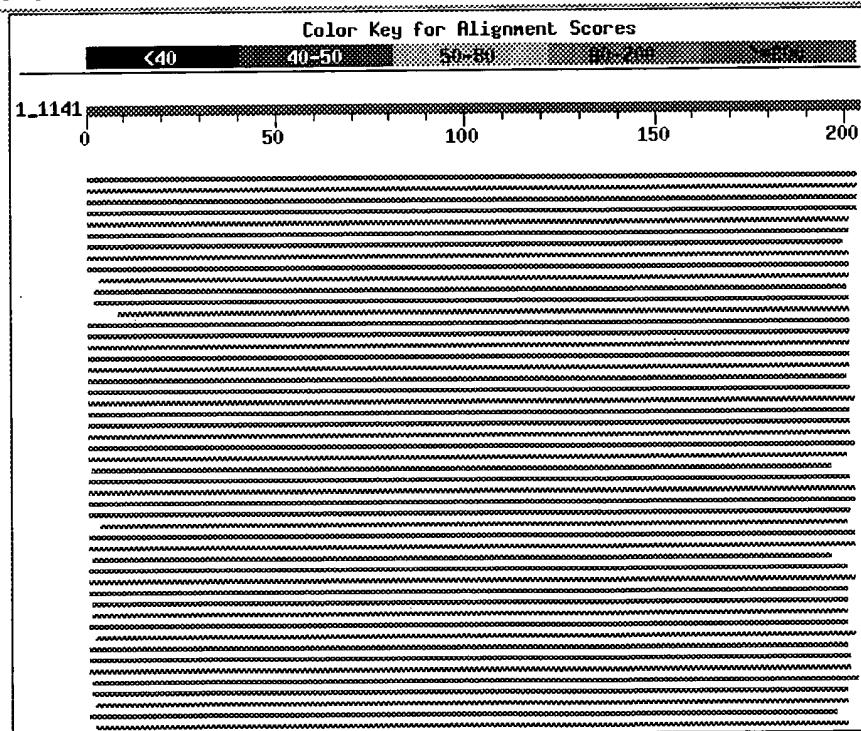
(204 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,475,854 sequences; 475,827,238 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports**Distribution of 100 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments

Related Structures

Score E

Sequences producing significant alignments:						(bits)	Value
gi	134649	sp	P28760	SODM_BACCA	Superoxide dismutase [Mn] >g...	373	e-103
gi	134650	sp	P00449	SODM_BACST	Superoxide dismutase [Mn] >g...	372	e-102
gi	7798571	dbj	BAA95631.1	superoxide dismutase [Geobacillu...		369	e-101
gi	448837	prf	1918164A	superoxide dismutase		367	e-101
gi	15613972	ref	NP_242275.1	superoxide dismutase [Bacillus...		311	4e-84
gi	16079557	ref	NP_390381.1	superoxide dismutase [Bacillus...		308	3e-83
gi	3355882	dbj	BAA31974.1	superoxide dismutase [Bacillus s...		308	3e-83
gi	32468794	emb	CAB14432.2	superoxide dismutase [Bacillus ...		307	7e-83
gi	3790114	emb	CAA05291.1	manganese superoxide dismutase [...		306	1e-82
gi	30264347	ref	NP_846724.1	superoxide dismutase, Mn [Baci...		306	2e-82
gi	23200182	pdb	1JR9_A	Chain A, Crystal Structure Of Mangan...		303	1e-81
gi	23099387	ref	NP_692853.1	manganese superoxide dismutase...		302	3e-81
gi	30022355	ref	NP_833986.1	Superoxide dismutase [Mn] [Bac...		298	2e-80
gi	16800546	ref	NP_470814.1	superoxide dismutase [Listeria...		285	4e-76
gi	29375094	ref	NP_814247.1	superoxide dismutase, Mn [Ente...		282	2e-75
gi	16803479	ref	NP_464964.1	superoxide dismutase [Listeria...		282	2e-75
gi	7433329	pir	S20019	superoxide dismutase (EC 1.15.1.1) (...		281	5e-75
gi	134666	sp	P28763	SODM_LISIV	Superoxide dismutase [Mn] >g...	276	1e-73
gi	3320377	gb	AAC26483.1	manganese superoxide dismutase [V...		276	2e-73
gi	18378721	gb	AAL68691.1	AF462457_1 superoxide dismutase [...		268	5e-71
gi	32492801	gb	AAP85516.1	SodA [Aeromonas salmonicida subs...		264	6e-70
gi	8977980	emb	CAB95744.1	superoxide dismutase [Staphyloco...		264	7e-70
gi	27468158	ref	NP_764795.1	superoxide dismutase SodA [Sta...		263	1e-69
gi	15924543	ref	NP_372077.1	superoxide dismutase [Staphylo...		263	2e-69
gi	15599664	ref	NP_253158.1	superoxide dismutase [Pseudomo...		262	3e-69
gi	11121341	emb	CAC14833.1	superoxide dismutase [Staphyloc...		261	3e-69
gi	17227566	ref	NP_484114.1	superoxide dismutase [Nostoc s...		260	8e-69
gi	23135202	ref	ZP_00116957.1	hypothetical protein [Cytoph...		258	4e-68
gi	1084032	pir	A53294	superoxide dismutase (EC 1.15.1.1) (...		257	1e-67
gi	21231716	ref	NP_637633.1	superoxide dismutase [Xanthomo...		255	3e-67
gi	31074373	gb	AAP41921.1	Mn/Fe superoxide dismutase [Chlo...		255	3e-67
gi	23126478	ref	ZP_00108372.1	hypothetical protein [Nostoc...		255	3e-67
gi	21243120	ref	NP_642702.1	superoxidase dismutase [Xantho...		254	4e-67
gi	1150790	gb	AAB47971.1	superoxide dismutase [Xanthomonas...		254	5e-67
gi	23200074	pdb	1GV3_A	Chain A, The 2.0 Angstrom Resolution...		254	6e-67
gi	1711423	sp	P50059	SOD2_PLEBO	Superoxide dismutase [Mn] 2...	251	6e-66
gi	1711456	sp	P09214	SODM_THETH	Superoxide dismutase [Mn] >...	251	6e-66
gi	23061777	ref	ZP_00086602.1	hypothetical protein [Pseudo...		251	7e-66
gi	77595	pir	S07147	superoxide dismutase (EC 1.15.1.1) (Mn...		251	7e-66
gi	23470984	ref	ZP_00126316.1	hypothetical protein [Pseudo...		251	7e-66
gi	26987682	ref	NP_743107.1	superoxide dismutase (Mn) [Pse...		250	1e-65
gi	134640	sp	P23744	SODF_METJ	Superoxide dismutase [Mn-Fe] ...	249	2e-65
gi	2500831	sp	P77929	SODM_PSEPU	Superoxide dismutase [Mn] >...	248	4e-65
gi	32474407	ref	NP_867401.1	superoxide dismutase, Mn famil...		246	1e-64
gi	15806297	ref	NP_295003.1	superoxide dismutase (sodA), M...		246	2e-64
gi	1711422	sp	P50058	SOD1_PLEBO	Superoxide dismutase [Mn] 1...	244	5e-64
gi	1711455	sp	P53653	SODM_THEAQ	Superoxide dismutase [Mn] >...	244	6e-64
gi	30023475	ref	NP_835106.1	Superoxide dismutase [Mn] [Bac...		243	1e-63
gi	21397929	ref	NP_653914.1	sodfe_C, Iron/manganese supero...		242	2e-63
gi	22996085	ref	ZP_00040357.1	hypothetical protein [Xylell...		242	3e-63
gi	22995080	ref	ZP_00039563.1	hypothetical protein [Xylell...		241	6e-63
gi	24182472	gb	AAN16456.2	manganese-containing superoxide ...		240	8e-63
gi	32035144	ref	ZP_00135190.1	hypothetical protein [Actino...		239	2e-62
gi	28199854	ref	NP_780168.1	superoxide dismutase [Xylella ...		238	4e-62
gi	15923123	ref	NP_370657.1	superoxide dismutase [Staphylo...		237	8e-62
gi	16329169	gb	AAG44813.2	AF273269_1 superoxide dismutase [...		237	9e-62
gi	23040106	ref	ZP_00071638.1	hypothetical protein [Tricho...		236	1e-61
gi	1711438	sp	P53642	SODM_BORPE	Superoxide dismutase [Mn] >...	236	2e-61
gi	15839203	ref	NP_299891.1	superoxide dismutase [MN] [Xyl...		235	4e-61
gi	16124175	ref	NP_407488.1	superoxide dismutase [Mn] [Yer...		234	4e-61
gi	1711458	sp	P53655	SODM_YEREN	Superoxide dismutase [Mn] >...	234	7e-61
gi	21910607	ref	NP_664875.1	superoxide dismutase [Mn] [Str...		234	9e-61
gi	541376	pir	PN0614	superoxide dismutase (EC 1.15.1.1) (M...		233	1e-60

gi 23130308 ref ZP_00112125.1	hypothetical protein [Nostoc...	233	1e-60
gi 6094321 sp O30826 SODM_HAEDU	Superoxide dismutase [Mn] >...	233	2e-60
gi 33151556 ref NP_872909.1	manganese superoxide dismutase...	233	2e-60
gi 19746368 ref NP_607504.1	superoxide dismutase [Streptoc...	232	2e-60
gi 13959576 sp P77957 SODM_STRPY	Superoxide dismutase [Mn]	232	3e-60
gi 15804498 ref NP_290538.1	superoxide dismutase, manganese...	232	3e-60
gi 24115202 ref NP_709712.1	superoxide dismutase, manganese...	232	3e-60
gi 15551671 emb CAC69393.1	manganese superoxide dismutase...	231	5e-60
gi 15675326 ref NP_269500.1	superoxide dismutase (Fe/Mn) [...	231	5e-60
gi 16131748 ref NP_418344.1	superoxide dismutase, manganese...	231	5e-60
gi 2808462 emb CAAI1227.1	superoxide dismutase [Streptococ...	230	9e-60
gi 26250673 ref NP_756713.1	Superoxide dismutase [Mn] [Esc...	230	1e-59
gi 28871594 ref NP_794213.1	superoxide dismutase, Mn [Pseu...	230	1e-59
gi 16762379 ref NP_457996.1	manganese superoxide dismutase...	230	1e-59
gi 16767321 ref NP_462936.1	superoxide dismutase, manganese...	229	2e-59
gi 15672390 ref NP_266564.1	superoxide dismutase [Lactococ...	229	2e-59
gi 3212626 pdb 1VEW A	Chain A, Manganese Superoxide Dismuta...	229	2e-59
gi 808038 gb AAC43331.1	Mn-superoxide dismutase	228	3e-59
gi 13399622 pdb 1I0H A	Chain A, Crystal Structure Of The E...	228	5e-59
gi 14719524 pdb 1EN5 A	Chain A, Crystal Structure Analysis ...	228	5e-59
gi 2500830 sp Q59679 SODM_PASHA	Superoxide dismutase [Mn] >...	227	7e-59
gi 32029513 ref ZP_00132526.1	hypothetical protein [Haemop...	227	7e-59
gi 541031 pir PN0615	superoxide dismutase (EC 1.15.1.1) (F...	226	1e-58
gi 14719520 pdb 1EN4 A	Chain A, Crystal Structure Analysis ...	226	1e-58
gi 14719528 pdb 1EN6 A	Chain A, Crystal Structure Analysis ...	226	1e-58
gi 22135437 gb AAM93199.1	superoxide dismutase [Thermus an...	226	1e-58
gi 22135443 gb AAM93202.1	superoxide dismutase [Thermus fi...	226	2e-58
gi 13399618 pdb 1I08 A	Chain A, Crystal Structure Analysis ...	226	2e-58
gi 17226292 gb AAL37717.1 AF413524_1	superoxide dismutase [...]	226	2e-58
gi 22135445 gb AAM93203.1	superoxide dismutase [Thermus os...	224	4e-58
gi 3334336 sp Q42684 SODM_CHLRE	Superoxide dismutase [Mn], ...	224	6e-58
gi 5758312 gb AAD50778:1 AF162664_1	manganese co-factored s...	224	6e-58
gi 22135439 gb AAM93200.1	superoxide dismutase [Thermus br...	224	7e-58
gi 22135441 gb AAM93201.1	superoxide dismutase [Thermus ig...	224	8e-58
gi 22135447 gb AAM93204.1	superoxide dismutase [Thermus sc...	224	9e-58
gi 15900660 ref NP_345264.1	superoxide dismutase, manganese...	224	9e-58
gi 22536952 ref NP_687803.1	superoxide dismutase, Fe-Mn [S...	223	1e-57

Alignments

 Get selected sequences Select all Deselect all

>gi|134649|sp|P28760|SODM_BACCA Superoxide dismutase [Mn]
 gi|98098|pir|S22053 superoxide dismutase (EC 1.15.1.1) (Mn) - Bacillus caldotenax
 gi|39453|emb|CAA44556.1| manganese superoxide dismutase [Bacillus caldotenax]
 gi|7578509|gb|AAF64074.1|AF147780_1 superoxide dismutase [Geobacillus thermoleovo]
 gi|384175|prf|1905285A superoxide dismutase
 Length = 204

Score = 373 bits (958), Expect = e-103
 Identities = 189/204 (92%), Positives = 189/204 (92%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQNKXXXXXXXXX 60
 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQNK
 Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQNKSLLELLSN 60

Query: 61 XXXXXXXIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS
 Sbjct: 61 LEALPESIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120

Query: 121 KAAAGRFGSGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
 KAAAGRFGSGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE

Sbjct: 121 KAAAGRGSGWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180

Query: 181 YIAAFWNIVNWDEVAKRYSEAKAK 204

YIAAFWNIVNWDEVAKRYSEAKAK

Sbjct: 181 YIAAFWNIVNWDEVAKRYSEAKAK 204

>gi|134650|sp|P00449|SODM_BACST Superoxide dismutase [Mn]
gi|1070456|pir|DSBSNF superoxide dismutase (EC 1.15.1.1) (Mn) - *Bacillus stearothermophilus*
gi|143203|gb|AAA22600.1| manganese superoxide dismutase (EC 1.15.1.1)
gi|143552|gb|AAA22765.1| Mn-superoxide dismutase
gi|143555|gb|AAA22767.1| Mn-superoxide dismutase
Length = 204

Score = 372 bits (954), Expect = e-102

Identities = 187/204 (91%), Positives = 189/204 (92%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNK

Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNK SLEELLSN 60

Query: 61 XXXXXXXXIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120
IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELA+AINKKFGSFTAFKDEFS

Sbjct: 61 LEALPESIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELADAINKKFGSFTAFKDEFS 120

Query: 121 KAAAGRGSGWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
KAAAGRGSGWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE

Sbjct: 121 KAAAGRGSGWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180

Query: 181 YIAAFWNIVNWDEVAKRYSEAKAK 204

YIAAFWN+VNWDEVAKRYSEAKAK

Sbjct: 181 YIAAFWNVNWDEVAKRYSEAKAK 204

>gi|7798571|dbj|BAA95631.1| superoxide dismutase [Geobacillus thermoleovorans]
Length = 204

Score = 369 bits (946), Expect = e-101

Identities = 187/204 (91%), Positives = 187/204 (91%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60

MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNK

Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNK SLEELLSN 60

Query: 61 XXXXXXXXIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120
IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS

Sbjct: 61 LEALPESIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120

Query: 121 KAAAGRGSGWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
KAAAGRF GWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE

Sbjct: 121 KAAAGRFSPGWAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180

Query: 181 YIAAFWNIVNWDEVAKRYSEAKAK 204

YIAAFWNIVNWDEVAKRYSEAKAK

Sbjct: 181 YIAAFWNIVNWDEVAKRYSEAKAK 204

>gi|448837|prf||1918164A superoxide dismutase
Length = 205

Score = 367 bits (941), Expect = e-101

Identities = 187/205 (91%), Positives = 189/205 (92%), Gaps = 1/205 (0%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNK

Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNK SLEELLSN 60

Query: 61 XXXXXXXIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELA+AINKKFGSFTAFKDEFS

Sbjct: 61 LEALPESIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELADAINKKFGSFTAFKDEFS 120

Query: 121 KAAAGRGSGGAWLVNNGELEITSTPNQDS-PIMEGKTPILGLDVWEHAYYLKYQNRRP 179
 KAAAGRGSGGAWLVNNGELEITSTPNQDS PIMEGKTPILGLDVWEHAYYLKYQNRRP

Sbjct: 121 KAAAGRGSGGAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRP 180

Query: 180 YIAAFWNIVNWDEVAKRYSEAKAK 204
 YIAAFWN+VNWDEVAKRYSEAKAK

Sbjct: 181 YIAAFWNVNWDEVAKRYSEAKAK 205

>gi|15613972|ref|NP_242275.1| superoxide dismutase [Bacillus halodurans]
gi|25285807|pir|A83826 superoxide dismutase sodA [imported] - Bacillus halodurans
 C-125)
gi|10174025|dbj|BAB05128.1| superoxide dismutase [Bacillus halodurans]
 Length = 202

Score = 311 bits (798), Expect = 4e-84

Identities = 153/202 (75%), Positives = 169/202 (83%)

Query: 1 MPFELPALPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
 M FELP LPYP +ALEPHID+ TMNIHH KHHNTYVT LNAALEGH L K

Sbjct: 1 MAFELPKLPY PANALEPHIDEATMNIHHGKHHNTYVTKLNAALEGH S A E K S I E A L V S D 60

Query: 61 XXXXXXXIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNGGGHANH+LFW ILSPNGGG PTGELA+AIN +FGSF FK++F+

Sbjct: 61 LDAVPENIRTA VRNNGGGHANHTLFWQILSPNGGAPGTGELADAINEAFGSFDQFKEKFA 120

Query: 121 KAAAGRGSGGAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRP 180
 AAA RFGSGGAWLVNN+G+LEITSTPNQD+P+MEGKTPILGLDVWEHAYYL YQNRRP+

Sbjct: 121 DAAANRGSGGAWLVVNDGKLEITSTPNQDTPLMEGKTPILGLDVWEHAYYLNYQNRRPD 180

Query: 181 YIAAFWNIVNWDEVAKRYSEAK 202

YI+AFWN+VNWDEVAKRY+EAK

Sbjct: 181 YISAFWNVNWDEVAKRYNEAK 202

>gi|16079557|ref|NP_390381.1| superoxide dismutase [Bacillus subtilis]
gi|1711437|sp|P54375|SODM_BACSU Superoxide dismutase [Mn] (General stress protein
gi|7433327|pir|B69709 superoxide dismutase (EC 1.15.1.1) (Mn) sodA - Bacillus su
gi|1303851|dbj|BAA12507.1| YggD [Bacillus subtilis]
 Length = 226

Score = 308 bits (790), Expect = 3e-83

Identities = 152/200 (76%), Positives = 166/200 (83%)

Query: 1 MPFELPALPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
 M +ELP LPY YDALEPHIDKETM IHHTKHHNTYVTNLNA A+EG+ L NK

Sbjct: 1 MAYELPELPYAYDALEPHIDKETMTIHHTKHHNTYVTNLNAVEGNTALANKSVEELVAD 60

Query: 61 XXXXXXXIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNGGGHANH LFWT+LSPNGGEPGT LAE IN FGSF FK++F+

Sbjct: 61 LDSVPENIRTA VRNNGGGHANHKLFWTLLSPNGGEPGTGALAEINSVFGSFDKFKEQFA 120

Query: 121 KAAAGRGSGGAWLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRP 180
 AAAGRGSGGAWLVNNNG+LEITSTPNQDSP+ EGKTPILGLDVWEHAYYL YQNRRP+

Sbjct: 121 AAAAGRGS GGAWLVVNNNGKLEITSTPNQDSPLSEGKTPILGLDVWEHAYYLNYQNRRPD 180

Query: 181 YIAAFWNIVNWDEVAKRYSE 200

YI+AFWN+VNWDEVA+ YS+

Sbjct: 181 YISAFWNVNWDEVARLYSD 200

>gi|3355882|dbj|BAA31974.1| superoxide dismutase [Bacillus subtilis]
 Length = 202

Score = 308 bits (790), Expect = 3e-83
 Identities = 155/202 (76%), Positives = 168/202 (83%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
 M +ELP LPY YDALEPHIDKETM IHHTKHHNTYVTNLN A+EG+ L NK
 Sbjct: 1 MAYELPELPYAYDALEPHIDKETMTIHHTKHHNTYVTNLNKAVEGNTALANKSVEELVAD 60

Query: 61 XXXXXXXIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNGGGHANH LFWT+LSPNGGEPGTG LAE IN FGSF FK++F+
 Sbjct: 61 LDSVPENIRTA VRNNNGGGHANHKLFWTLLSPNGGEPGTGALAEINSVFGSF DFKKEQFA 120

Query: 121 KAAAGRFGSGWA LWVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
 AAAGRFGSGWA LWVNNG+LEITSTPNQDSP+ EGKTPILGLDVWEHAYYL YQNRRP+
 Sbjct: 121 AAAAGRFGSGWA LWVNNGKLEITSTPNQDSPSEGKTPILGLDVWEHAYYLNYQNRRPD 180

Query: 181 YIAAFWNIVNWDEVA KRYSEAK 202
 YI+AFWN+VNWDEVA+ YSEAK
 Sbjct: 181 YISAFWNVNVNWD EVA RLYSEAK 202

>gi|32468794|emb|CAB14432.2| superoxide dismutase [Bacillus subtilis subsp. subtilis] Length = 202

Score = 307 bits (786), Expect = 7e-83
 Identities = 154/202 (76%), Positives = 167/202 (82%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
 M +ELP LPY YDALEPHIDKETM IHHTKHHNTYVTNLN A+EG+ L NK
 Sbjct: 1 MAYELPELPYAYDALEPHIDKETMTIHHTKHHNTYVTNLNKAVEGNTALANKSVEELVAD 60

Query: 61 XXXXXXXIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNGGGHANH LFWT+LSPNGGEPGTG LAE IN FGSF FK++F+
 Sbjct: 61 LDSVPENIRTA VRNNNGGGHANHKLFWTLLSPNGGEPGTGALAEINSVFGSF DFKKEQFA 120

Query: 121 KAAAGRFGSGWA LWVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
 AAAGRFGSGWA LWVNNG+LEITSTPNQDSP+ EGKTPILGLDVWEHAYYL YQNRRP+
 Sbjct: 121 AAAAGRFGSGWA LWVNNGKLEITSTPNQDSPSEGKTPILGLDVWEHAYYLNYQNRRPD 180

Query: 181 YIAAFWNIVNWDEVA KRYSEAK 202
 YI+AFWN+VNWDEVA+ YSE K
 Sbjct: 181 YISAFWNVNVNWD EVA RLYSERK 202

>gi|3790114|emb|CAA05291.1| manganese superoxide dismutase [Bacillus licheniformis] Length = 202

Score = 306 bits (785), Expect = 1e-82
 Identities = 155/202 (76%), Positives = 167/202 (82%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXX 60
 M ++LP LPY YDALEPHIDKETMNIHHTKHHNTYVT LN A+ G DL++K
 Sbjct: 1 MAYKLPELPYAYDALEPHIDKETMNIHHTKHHNTYVTKLNEAVAGKQDLESKSVEELVAN 60

Query: 61 XXXXXXXIRTAVRNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFS 120
 IRTAVRNNGGGHANHSLFW +LSPNGGG PTGELAEAIN KFGSF FK++F+
 Sbjct: 61 LDAVPENIRTA VRNNNGGGHANHSLFWKLLSPNGGGAPTGELAEAINS KFGSF DQFKEDFA 120

Query: 121 KAAAGRFGSGWA LWVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
 AAA RFGSGWA LWVNNGELEITSTPNQDSP+ EGKTPILGLDVWEHAYYL YQNRRP+
 Sbjct: 121 AAAAARFGSGWA LWVNNGELEITSTPNQDSPSEGKTPILGLDVWEHAYYLNYQNRRPD 180

Query: 181 YIAAFWNIVNWDEVA KRYSEAK 202
 YI AFWN+VNWDEVA YSEAK
 Sbjct: 181 YIKAFWNVNVNWD EVA PLYSEAK 202

>gi|30264347|ref|NP_846724.1| superoxide dismutase, Mn [Bacillus anthracis str. Ames]
 >gi|30259005|gb|AAP28210.1| superoxide dismutase, Mn [Bacillus anthracis str. Ames]

Length = 203

Score = 306 bits (783), Expect = 2e-82
 Identities = 149/199 (74%), Positives = 164/199 (82%)

Query: 4 ELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXXXXX 63
 ELP LPY YDALEPH DKETMNIHHTKHHNTY+TNLNAALEGH +L +K
 Sbjct: 5 ELPNLPYAYDALEPHFDKETMNIHHTKHHNTYITNLNAALEGHAELADKSVEELVANLNE 64

Query: 64 XXXXIRTAVRNNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFSKA 123
 IRTAVRNNNGGGHANH+ FWTLSPNGGG+P GELA AI KFGSF AFK+EF+KA
 Sbjct: 65 VPEAIRTAVRNNNGGGHANHTFFWTILSPNGGQPVGELATAIEAKFGSFDAFKEEFAKAG 124

Query: 124 AGRFGSGWAWLVVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPEYIA 183
 A RFGSGWAWLVVNNGELEITSTPNQDSP+ EGKTP++GLDVWEHAYYL YQNRRP+YI
 Sbjct: 125 ATRFGSGWAWLVVNNGELEVSTPNQDSPMLEGKTPVIGLDVWEHAYYLNYQNRRPDYIG 184

Query: 184 AFWNIVNWDEVAKRYSEAK 202
 AFWN+V+W+ KRY EAK
 Sbjct: 185 AFWNVVDWNAAEKRYQEAK 203

>gi|23200182|pdb|1JR9|A Chain A, Crystal Structure Of Manganese Superoxide Dism
 Bacillus Halodenitrificans
 Length = 202

Score = 303 bits (776), Expect = 1e-81
 Identities = 149/199 (74%), Positives = 168/199 (84%)

Query: 3 FELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXXXXX 62
 FELP LPY YDALEP IDKETMNIHHTKHHNTYVT LN ALEGH DL+NK
 Sbjct: 3 FELPELPYAYDALEPTIDKETMNIHHTKHHNTYVTKLNGALEGHEDLKNKSLNDLISNLD 62

Query: 63 XXXXIRTAVRNNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFSKA 122
 IRTAVRNNNGGGHANHSLFW ++SPNGGG+PTGE+A+ IN K+GSF F++EF+ A
 Sbjct: 63 AVPENIRTAVRNNNGGGHANHSLFWKLMSPNGGGKPTGEVADKINDKYGSFEKFQEEFAAA 122

Query: 123 AAGRFGSGWAWLVVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPEYI 182
 AAGRFGSGWAWLVVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQN+RP+YI
 Sbjct: 123 AAGRFGSGWAWLVVNNGEIEIMSTPIQDNPLMEGKKPILGLDVWEHAYYLKYQNKRPDYI 182

Query: 183 AAFWNIVNWDEVAKRYSEA 201
 +AFWN+VNWDEVA +YS+A
 Sbjct: 183 SAFWNVVNWDEVAAQYSQA 201

>gi|23099387|ref|NP_692853.1| manganese superoxide dismutase [Oceanobacillus ihe
 gi|22777616|dbj|BAC13888.1| manganese superoxide dismutase [Oceanobacillus iheyen
 Length = 203

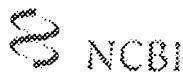
Score = 302 bits (773), Expect = 3e-81
 Identities = 156/200 (78%), Positives = 169/200 (84%)

Query: 3 FELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQNKXXXXXXXXXXXX 62
 FELP LPY YDALEP IDKETMNIHHTKHHNTYVT LN ALEGH DLQ+K
 Sbjct: 4 FELPELPYAYDALEPTIDKETMNIHHTKHHNTYVTKLNALEGHADLQSKSVEELISNLD 63

Query: 63 XXXXIRTAVRNNNGGGHANHSLFWTILSPNGGEPGTGELAEAINKKFGSFTAFKDEFSKA 122
 +TAVRNNNGGGHANHSLFW +LSPNGGEPGTGELA+ IN KFGS FK+EF+ A
 Sbjct: 64 AVPENAKTAVRNNNGGGHANHSLFWKLLSPNGGEPGTGELADKINAKFGSLDKFKEEFAAA 123

Query: 123 AAGRFGSGWAWLVVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPEYI 182
 AAGRFGSGWAWL+VNNGELEITSTPNQDSP+MEGKTP+LGLDVWEHAYYLKYQN+RPEYI
 Sbjct: 124 AAGRFGSGWAWLIVVNNGELEITSTPNQDSPMLEGKTPVGLDVWEHAYYLKYQNKRPEYI 183

Query: 183 AAFWNIVNWDEVAKRYSEA 202
 +AFWN+VNWDEVAKRYSEA +YS+A



NCBI Conserved Domain Search

New Search PubMed Nucleotide Protein Structure CDD Taxonomy Help?

RPS-BLAST 2.2.6 [Apr-09-2003]

Query: local sequence:
(204 letters)

Database: #cdd.v1.62
11,088 PSSMs; 2,717,223 total columns

Click on boxes for multiple alignments



Show Domain Relatives

- This CD alignment includes 3D structure. To display structure, download [Cn3D](#)!

PSSMs producing significant alignments:

Score E
(bits) value

- gnl|CDD|10475 COG0605, SodA, Superoxide dismutase [Inorganic ion transport a... 282 3e-77
- gnl|CDD|17208 pfam02777, sodfe_C, Iron/manganese superoxide dismutases, C-te... 181 7e-47
- gnl|CDD|15113 pfam00081, sodfe, Iron/manganese superoxide dismutases, alpha-... 106 1e-24

- gnl|CDD|10475, COG0605, SodA, Superoxide dismutase [Inorganic ion transport and metabolism]

CD-Length = 204 residues, 99.5% aligned
Score = 282 bits (722), Expect = 3e-77

Query: 1	MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHHPDLQNKSLEELLSN	60
Sbjct: 2	MAYELPELPYAYDALEPHISARTMELHHDKHHQTYVNNLNAALEGLTE---ELEDLSLEE	58
Query: 61	LEALPESIRTAVRNNNGGHANHNSLFWTILSPN-GGGEPTGELAAEAINKKGSFTAFKDEF	119
Sbjct: 59	I IKKLAGLPAALFNNAGGHWNHSLFWENLSPGGGGKPTGELAAAINKDFGSFDKFKEEF	118
Query: 120	SKAAAGRFGSGWAWLVVN-NGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRR	178
Sbjct: 119	TAAAASVFGSGWAWLVYDPDGKLEIVSTYNQDTPLMWGSVPILLGDVWEHAYLDYGNRR	178
Query: 179	PEYIAAFWNIVNWDEVAKRYSEAKAK	204
Sbjct: 179	PDYVEAFWNVVNWDEVEEFEEAKKE	204

- gnl|CDD|17208, pfam02777, sodfe_C, Iron/manganese superoxide dismutases, C-terminal domain. superoxide dismutases (SODs) catalyse the conversion of superoxide radicals to molecular oxygen. Three evolutionarily distinct families of SODs are known, of which the Mn/Fe-binding family is one. In humans, there is a cytoplasmic Cu/Zn SOD, and a mitochondrial Mn/Fe SOD. C-terminal domain is a mixed alpha/beta fold.

CD-Length = 111 residues, 100.0% aligned
Score = 181 bits (460), Expect = 7e-47

Query: 95 GEPTGELAEAINKFGSFTAFKDEFSKAAAGRPGSGWAWLVVNN--GELEITSTPNQDSP 152
Sbjct: 1 GEPTGELADAIDEDFGSFKEKFKEEFTAAAAGVFGSGWAWLVYDNEGKKLAIVSTPNQDNP 60

Query: 153 IMEGKTPILGLDVWEHAYYLKYQNRRPEYIAAFWNIVNWDEVAKRYSEAKA 203
Sbjct: 61 LTEGLTPLLGLDVWEHAYYLKYQNRRFDYLKAFWNVNVNWDDEVSKRFEAKK 111

• gnl|CDD|15113, pfam00081, sodfe, Iron/manganese superoxide dismutases, alpha-hairpin domain. superoxide dismutases (SODs) catalyse the conversion of superoxide radicals to molecular oxygen. Three evolutionarily distinct families of SODs are known, of which the Mn/Fe-binding family is one. In humans, there is a cytoplasmic Cu/Zn SOD, and a mitochondrial Mn/Fe SOD. N-terminal domain is a long alpha antiparallel hairpin. A small fragment of YTRE_LEPBI matches well - sequencing error?

CD-Length = 83 residues, 100.0% aligned
Score = 106 bits (267), Expect = 1e-24

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDQLQNKSLEELLSN 60
Sbjct: 1 MKYRLPPPLPYDYDALEPHISKEITLEFHNGKHHQTYVNNLNAALEGLEEARKK-----L 53

Query: 61 LEALPESIRTAVRNNNGGGHANHSLFWTILS 90
Sbjct: 54 EELIIAALQGALRNNGGGHWNHTLFWKNLS 83

[Help](#) | [Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

RID: 1059166006-9282-7710.BLASTQ1

Query=

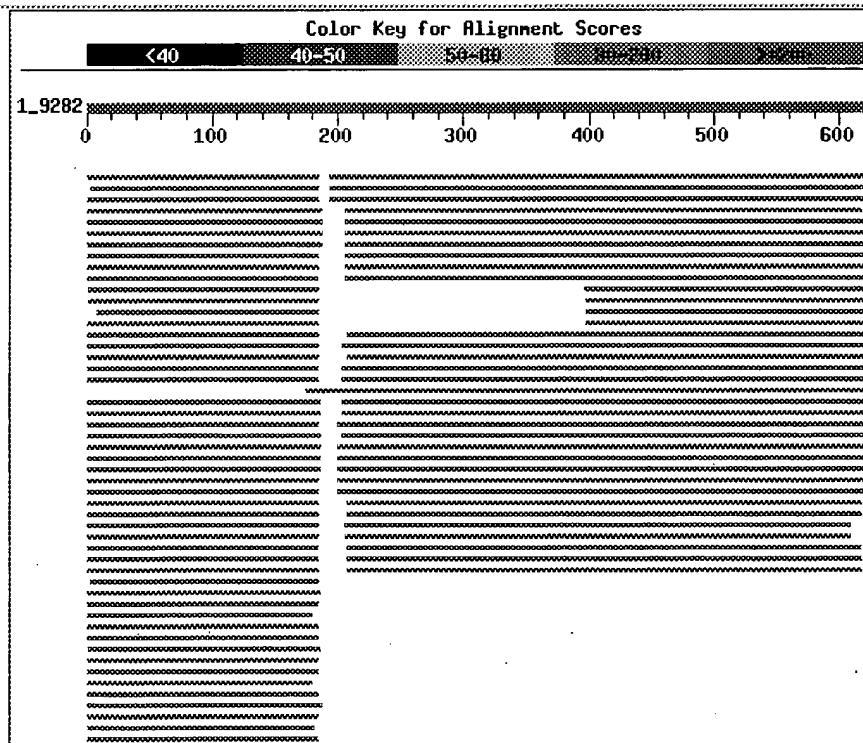
(622 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
 1,475,854 sequences; 475,827,238 total letters

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Related Structures

Sequences producing significant alignments:	Score (bits)	E Value
gi 529984 gb AAA23210.1 neurotoxin type F >gi 971349 emb C...	756	0.0
gi 3805790 emb CAA73972.1 botT [Clostridium botulinum]	654	0.0
gi 399137 sp P30996 BXF_CLOBO Botulinum neurotoxin type F p...	645	0.0
gi 479333 pir S33411 botulinum neurotoxin type F - Clostri...	593	e-168
gi 9650999 dbj BAB03512.1 type E botulinum toxin [Clostrid...	565	e-160
gi 98569 pir S21178 botulinum neurotoxin type E precursor ...	564	e-159
gi 399135 sp Q00496 BXE_CLOBO Botulinum neurotoxin type E p...	563	e-159
gi 399136 sp P30995 BXE_CLOBU Botulinum neurotoxin type E p...	559	e-158

gi 9955895 dbj BAB12249.1	type E botulinum toxin [Clostridium botulinum type E]	559	e-158
gi 21832314 dbj BAC05434.1	type E botulinum toxin [Clostridium botulinum type E]	559	e-158
gi 1084233 pir S48110	neurotoxin type F - Clostridium botulinum neurotoxin type F	392	e-107
gi 134649 sp P28760 SODM_BACCA	Superoxide dismutase [Mn] >g...	387	e-106
gi 134650 sp P00449 SODM_BACST	Superoxide dismutase [Mn] >g...	386	e-106
gi 7798571 dbj BAA95631.1	superoxide dismutase [Geobacillus sp.]	382	e-105
gi 448837 prf 1918164A	superoxide dismutase	381	e-104
gi 7438650 pir S48109	neurotoxin type F - Clostridium botulinum neurotoxin type F	330	3e-89
gi 15613972 ref NP_242275.1	superoxide dismutase [Bacillus subtilis]	327	4e-88
gi 30264347 ref NP_846724.1	superoxide dismutase, Mn [Bacillus subtilis]	318	2e-85
gi 3790114 emb CAA05291.1	manganese superoxide dismutase [...]	315	1e-84
gi 3355882 dbj BAA31974.1	superoxide dismutase [Bacillus subtilis]	315	1e-84
gi 32468794 emb CAB14432.2	superoxide dismutase [Bacillus subtilis]	313	5e-84
gi 16079557 ref NP_390381.1	superoxide dismutase [Bacillus subtilis]	312	1e-83
gi 23099387 ref NP_692853.1	manganese superoxide dismutase	311	2e-83
gi 23200182 pdb 1JR9 A	Chain A, Crystal Structure Of Manganese Superoxide Dismutase	310	4e-83
gi 30022355 ref NP_833986.1	Superoxide dismutase [Mn] [Bacillus subtilis]	308	2e-82
gi 407787 emb CAA50146.1	botulinum neurotoxin type E [Clostridium botulinum type E]	298	1e-79
gi 1084230 pir S48106	neurotoxin type E - Clostridium botulinum neurotoxin type E	297	4e-79
gi 16800546 ref NP_470814.1	superoxide dismutase [Listeria monocytogenes]	293	6e-78
gi 2499920 sp Q60393 BXG_CLOBO	Botulinum neurotoxin type G	292	1e-77
gi 29375094 ref NP_814247.1	superoxide dismutase, Mn [Enterococcus faecalis]	292	1e-77
gi 629166 pir S39791	neurotoxin - Clostridium botulinum	291	2e-77
gi 15419708 gb AAK97132.1	neurotoxin type B [Clostridium botulinum type B]	291	2e-77
gi 15982937 gb AAL11498.1	type B cryptic neurotoxin [Clostridium botulinum type B]	291	3e-77
gi 16803479 ref NP_464964.1	superoxide dismutase [Listeria monocytogenes]	291	3e-77
gi 3805785 emb CAA73968.1	bonT [Clostridium botulinum]	290	4e-77
gi 7433329 pir S20019	superoxide dismutase (EC 1.15.1.1) (Mn)	288	2e-76
gi 24137633 dbj BAC22064.1	neurotoxin [Clostridium botulinum]	288	3e-76
gi 3320377 gb AAC26483.1	manganese superoxide dismutase [Vibrio cholerae]	284	3e-75
gi 134666 sp P28763 SODM_LISIV	Superoxide dismutase [Mn] >g...	284	3e-75
gi 399134 sp P10844 BXB_CLOBO	Botulinum neurotoxin type B p...	280	4e-74
gi 11514111 pdb 1EPW A	Chain A, Crystal Structure Of Clostridium botulinum neurotoxin type A	280	5e-74
gi 15599664 ref NP_253158.1	superoxide dismutase [Pseudomonas aeruginosa]	280	6e-74
gi 18251976 gb AAL66183.1 AF464912_1	neurotoxin type A LHn	279	1e-73
gi 2118642 pir I40631	non-proteolytic botulinum neurotoxin	278	1e-73
gi 399133 sp P10845 BXA1_CLOBO	Botulinum neurotoxin type A	278	2e-73
gi 6137387 pdb 3BTA A	Chain A, Crystal Structure Of Botulinum neurotoxin type A	278	2e-73
gi 279630 pir BTCLAB	bontoxilysin (EC 3.4.24.69) A precursor	278	2e-73
gi 40382 emb CAA36289.1	type A neurotoxin (AA 1-1296) [Clostridium botulinum type A]	278	2e-73
gi 1084032 pir A53294	superoxide dismutase (EC 1.15.1.1) (Mn)	275	1e-72
gi 23135202 ref ZP_00116957.1	hypothetical protein [Cytophaga hutchinsonii]	274	3e-72
gi 32492801 gb AAP85516.1	SodA [Aeromonas salmonicida subspecies salmonicida]	274	4e-72
gi 21231716 ref NP_637633.1	superoxide dismutase [Xanthomonas campestris]	272	1e-71
gi 21243120 ref NP_642702.1	superoxidase dismutase [Xanthomonas campestris]	271	2e-71
gi 1150790 gb AAB47971.1	superoxide dismutase [Xanthomonas campestris]	271	2e-71
gi 31074373 gb AAP41921.1	Mn/Fe superoxide dismutase [Chlorobacterus sp.]	270	4e-71
gi 26987682 ref NP_743107.1	superoxide dismutase (Mn) [Pseudomonas aeruginosa]	270	4e-71
gi 18378721 gb AAL68691.1 AF462457_1	superoxide dismutase [Clostridium botulinum type B]	269	1e-70
gi 2500831 sp P77929 SODM_PSEPU	Superoxide dismutase [Mn] >g...	268	3e-70
gi 8977980 emb CAB95744.1	superoxide dismutase [Staphylococcus aureus]	267	3e-70
gi 1711456 sp P09214 SODM_THETH	Superoxide dismutase [Mn] >g...	266	6e-70
gi 27468158 ref NP_764795.1	superoxide dismutase SodA [Staphylococcus aureus]	266	8e-70
gi 77595 pir S07147	superoxide dismutase (EC 1.15.1.1) (Mn)	266	9e-70
gi 15924543 ref NP_372077.1	superoxide dismutase [Staphylococcus aureus]	266	9e-70
gi 23126478 ref ZP_00108372.1	hypothetical protein [Nostoc sp.]	266	1e-69
gi 23470984 ref ZP_00126316.1	hypothetical protein [Pseudomonas aeruginosa]	264	3e-69
gi 17227566 ref NP_484114.1	superoxide dismutase [Nostoc sp.]	263	7e-69
gi 23061777 ref ZP_00086602.1	hypothetical protein [Pseudomonas aeruginosa]	263	7e-69
gi 20137335 sp Q45894 BXA2_CLOBO	Botulinum neurotoxin type B	262	1e-68
gi 11121341 emb CAC14833.1	superoxide dismutase [Staphylococcus aureus]	261	3e-68
gi 15806297 ref NP_295003.1	superoxide dismutase (sodA), Mn	261	3e-68
gi 134640 sp P23744 SODF_METJ	Superoxide dismutase [Mn-Fe]	260	4e-68
gi 1711455 sp P53653 SODM_THEAQ	Superoxide dismutase [Mn] >g...	259	1e-67
gi 23200074 pdb 1GV3 A	Chain A, The 2.0 Angstrom Resolution	258	2e-67

gi 1711423 sp P50059 SOD2_PLEBO	Superoxide dismutase [Mn] 2...	258	2e-67
gi 32474407 ref NP_867401.1	superoxide dismutase, Mn famil...	257	4e-67
gi 2147809 pir S70582 botulinum neurotoxin type Dsa precur...		254	3e-66
gi 1711438 sp P53642 SODM_BORPE	Superoxide dismutase [Mn] >...	253	6e-66
gi 6939795 dbj EAA90661.1	neurotoxin [Clostridium botulinum]	252	1e-65
gi 15022165 gb AAK72964.2	tetanus toxin [Clostridium tetani]	252	2e-65
gi 22995080 ref ZP_00039563.1	hypothetical protein [Xylell...	251	2e-65
gi 28373188 ref NP_783831.1	tetanus toxin tetX [Clostridiu...	251	2e-65
gi 22996085 ref ZP_00040357.1	hypothetical protein [Xylell...	250	4e-65
gi 260239 gb AAB24244.1	type D neurotoxin [Bacteriophage d...	250	4e-65
gi 24182472 gb AAN16456.2	manganese-containing superoxide ...	250	6e-65
gi 32035144 ref ZP_00135190.1	hypothetical protein [Actino...	250	7e-65
gi 1711422 sp P50058 SOD1_PLEBO	Superoxide dismutase [Mn] 1...	249	1e-64
gi 4579738 dbj BAA75084.1	NTX [Clostridium botulinum D phage]	249	1e-64
gi 115188 sp P19321 BXD_CLOBO	Botulinum neurotoxin type D p...	248	2e-64
gi 28199854 ref NP_780168.1	superoxide dismutase [Xylella ...	246	6e-64
gi 15839203 ref NP_299891.1	superoxide dismutase [MN] [Xyl...	244	2e-63
gi 16124175 ref NP_407488.1	superoxide dismutase [Mn] [Yer...	243	7e-63
gi 30023475 ref NP_835106.1	Superoxide dismutase [Mn] [Bac...	243	9e-63
gi 541376 pir PN0614 superoxide dismutase (EC 1.15.1.1) (M...		243	1e-62
gi 1711458 sp P53655 SODM_YEREN	Superoxide dismutase [Mn] >...	243	1e-62
gi 23040106 ref ZP_00071638.1	hypothetical protein [Tricho...	242	1e-62
gi 15804498 ref NP_290538.1	superoxide dismutase, manganese...	242	1e-62
gi 15551671 emb CAC69393.1	manganese superoxide dismutase...	242	1e-62
gi 24115202 ref NP_709712.1	superoxide dismutase, manganese...	241	2e-62
gi 16329169 gb AAG44813.2 AF273269_1	superoxide dismutase [...]	241	2e-62
gi 16131748 ref NP_418344.1	superoxide dismutase, manganese...	241	2e-62

Alignments

Get selected sequences Select all Deselect all

>gi|529984|gb|AAA23210.1| neurotoxin type F
 gi|971349|emb|CAA57358.1| BoNT/F [Clostridium botulinum]
 Length = 1278

Score = 756 bits (1953), Expect = 0.0
 Identities = 403/429 (93%), Positives = 406/429 (94%), Gaps = 1/429 (0%)

Query: 194 LVPRGPGSKAPPRLCIRVNNRELFFVASESSYNENDINTPKIEDDTXXXXXXXXXXDEV 253
 ++PR G+KAPPRLCIRVNNRELFFVASESSYNENDINTPKIEDDTT DEV
 Sbjct: 432 VIPR-KGTKAPPRLCIRVNNRELFFVASESSYNENDINTPKIEDTTNLNNNYRNNLDEV 490

Query: 254 ILDYNSETIPQISNQLNTLVQDDSYVPRYDSNGTSEIEEHNVVDLNFFYLHAQKVPEG 313
 ILDYNSETIPQISNQLNTLVQDDSYVPRYDSNGTSEIEEHNVVDLNFFYLHAQKVPEG
 Sbjct: 491 ILDYNSETIPQISNQLNTLVQDDSYVPRYDSNGTSEIEEHNVVDLNFFYLHAQKVPEG 550

Query: 314 ETNISLTSSIDTALSEESQVYTFSSSEFINTINKPVHAALFISWINQVIRDFTEATQKS 373
 ETNISLTSSIDTALSEESQVYTFSSSEFINTINKPVHAALFISWINQVIRDFTEATQKS
 Sbjct: 551 ETNISLTSSIDTALSEESQVYTFSSSEFINTINKPVHAALFISWINQVIRDFTEATQKS 610

Query: 374 TFDKIADISLVVPYVGLALNIGNEVKENFKEAFELLGAGILLEFPELLIPTILVFTIK 433
 TFDKIADISLVVPYVGLALNIGNEVKENFKEAFELLGAGILLEFPELLIPTILVFTIK
 Sbjct: 611 TFDKIADISLVVPYVGLALNIGNEVKENFKEAFELLGAGILLEFPELLIPTILVFTIK 670

Query: 434 SFIGSSEXXXXXXXXXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNZ 493
 SFIGSSE SLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNZ
 Sbjct: 671 SFIGSENKNKIIKAINNSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNZ 730

Query: 494 VDAIKTVIEYKNNYTSDERNRLESEYNINNIREELNKKVSLAMENIERFITESSIFYLM 553
 VDAIKTVIEYKNNYTSDERNRLESEYNINNIREELNKKVSLAMENIERFITESSIFYLM
 Sbjct: 731 VDAIKTVIEYKNNYTSDERNRLESEYNINNIREELNKKVSLAMENIERFITESSIFYLM 790

Query: 554 KLINEAKVSKLREYDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYT 613
 KLINEAKVSKLREYDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYT
 Sbjct: 791 KLINEAKVSKLREYDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYT 850

Query: 614 NDKILILYF 622
 NDKILILYF
 Sbjct: 851 NDKILILYF 859

>gi|3805790|emb|CAA73972.1| bonT [Clostridium botulinum]
 Length = 1280

Score = 654 bits (1686), Expect = 0.0
 Identities = 347/429 (80%), Positives = 376/429 (87%), Gaps = 1/429 (0%)

Query: 194 LVPRGPGSKAPPRLCIRVNNRELFFVASESSYNENDINTPKEIDDTCXXXXXXXXXDEV 253
 ++PR G+K P LCIRVNNRELFFVASESSYNE+DINTPKEIDDTC DEV
 Sbjct: 432 IIPR-KGTQSPSLCIRVNNRELFFVASESSYNEDINTPKEIDDTCNLNNNYRNNLDEV 490

Query: 254 ILDYNSETIPQISNQLNTLVQDDSYVPRYDSNGTSEIEEHNVVDLNVFFYLHAQKVPEG 313
 ILDYNSETIPQISN+TLNTLVQD+SYVPRYDSNGTSEIEE++VVD NVFFYLHAQKVPEG
 Sbjct: 491 ILDYNSETIPQISNRTLNTLVQDNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKVPEG 550

Query: 314 ETNISLTSSIDTALSEESQVYTFSSSEFINTINKPVHAALFISWINQVIRDFTEATQKS 373
 ETNISLTSSIDTAL EES+VYTFSSSEFI+TINKPV+AALFI WI++VIRDFTEATQKS
 Sbjct: 551 ETNISLTSSIDTALLEESKVYTFSSSEFIDTINKPVNAALFIDWISKVIRDFTEATQKS 610

Query: 374 TFDKIADISLVVPYVGLALNIGNEVQKENFKEAFELLGAGILLEFVPELLIPTILVFTIK 433
 T DKIADISL+VPYVGLALNI E +K NF+EAPELLGAGILLEFVPEL IP ILVFTIK
 Sbjct: 611 TVDKIADISLVVPYVGLALNIVIEAEKGNFEEAFELLGAGILLEFVPELTIPVILVFTIK 670

Query: 434 SFIGSSEXXXXXXXXXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQ 493
 S+I S E SL+ERE KWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQ
 Sbjct: 671 SYIDSYENKNKAIAKAINNSLIERREAKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQ 730

Query: 494 VDAIKTVIEYKYNNTSDERNLESEYNINNIREELNKKVSLAMENIERFITESSIFYLM 553
 VDAIKT IEYKYNNTSDE+NRLES+YNINNI EELNKKVSLAM+NIERF+TESSI YLM
 Sbjct: 731 VDAIKTAIEYKYNNTSDEKNRLESKYNNINNIEELNKKVSLAMKNIERFMTESSISYLM 790

Query: 554 KLINEAKVSKLREYDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYT 613
 KLINEA+V KL+EYD+ VK LLDYI H+ ILG +EL DLVTSTLN+SIPFELSSYT
 Sbjct: 791 KLINEAEVGKLKEYDKHVKS DLLDYI LYHKLILGEQTKELEIDLVTSTLNNSIPFELSSYT 850

Query: 614 NDKILILYF 622
 NDKILI+YF
 Sbjct: 851 NDKILIYF 859

>gi|399137|sp|P30996|EXF_CLOBO Botulinum neurotoxin type F precursor (BoNT/F) (B
 gi|2118643|pir|I40813| neurotoxin type F - Clostridium botulinum
 gi|144867|gb|AAA23263.1| neurotoxin type F
 gi|383771|prf|1904210A| neurotoxin F
 Length = 1274

Score = 645 bits (1665), Expect = 0.0
 Identities = 347/429 (80%), Positives = 375/429 (87%), Gaps = 2/429 (0%)

Query: 194 LVPRGPGSKAPPRLCIRVNNRELFFVASESSYNENDINTPKEIDDTCXXXXXXXXXDEV 253
 ++PR G+KAPPRLCIRVNN ELFFVASESSYNE+DINTPKEIDDTC DEV
 Sbjct: 432 VIPR-KGTKAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTCNLNNNYRNNLDEV 490

Query: 254 ILDYNSETIPQISNQLNTLVQDDSYVPRYDSNGTSEIEEHNVVDLNVFFYLHAQKVPEG 313
 ILDYNSETIPQISN+TLNTLVQD+SYVPRYDSNGTSEIEE++VVD NVFFYLHAQKVPEG
 Sbjct: 491 ILDYNSETIPQISNRTLNTLVQDNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKVPEG 550

Query: 314 ETNISLTSSIDTALSEESQVYTFSSSEFINTINKPVHAALFISWINQVIRDFTEATQKS 373
 ETNISLTSSIDTAL EES+ FFSSEFI+TINKPV+AALFI WI++VIRDFTEATQKS

Sbjct: 551 ETNISLTSSIDTALLESK-DIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEATQKS 609

Query: 374 TFDKIADISLVPYVGLALNIGNEVQKENFKEAFELLGAGILLEFVPELLIPTILVFTIK 433
T DKIADISL+VPYVGLALNI E +K NF+EAPELLG GILLEFVPEL IP ILVFTIK

Sbjct: 610 TVDKIADISLIVPYVGLALNIIIEAEKGNFEEAFELLGVGILLEFVPELTIPVILVFTIK 669

Query: 434 SFIGSSEXXXXXXXXXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNZ 493
S+I S E SL+ERE KWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNZ

Sbjct: 670 SYIDSYENKNKAIKAINNSLIERREAKWEIYSWIVSNWLTRINTQFNKRKEQMYQALQNZ 729

Query: 494 VDAIKTVIEYKYNNTSDERNRLESEYNINNNIREELKKVSLAMENIERFITESSIFYLM 553
VDAIKT IEYKYNNTSDE+NRLESEYNINNI EELNKKVSLAM+NIERF+TESSI YLM

Sbjct: 730 VDAIKTAIEYKYNNTSDEKNRLESEYNINNIEELNKKVSLAMKNIERFMTTESSISYLM 789

Query: 554 KLINEAKVSKLREYDEGVKEYLLDYISEHRSILGSVQELNDLVTSTLNNSIPFELSSYT 613
KLINEAKV KL++YD VK LL+YI +HRSILG EL+DLVTSTLN+SIPFELSSYT

Sbjct: 790 KLINEAKVGKLKKYDNHVKS DLLNYILDHRSILGEQTNELSDLVTSTLNSSIPFELSSYT 849

Query: 614 NDKILILYF 622

NDKILI+YF

Sbjct: 850 NDKILIYF 858

>gi 479333 pir S33411	botulinum neurotoxin type F - Clostridium barati
gi 49139 emb CAA48329.1	neurotoxin type F [Clostridium baratii]
Length = 1268	

Score = 593 bits (1530), Expect = e-168
Identities = 314/414 (75%), Positives = 355/414 (85%), Gaps = 1/414 (0%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKEIDDTRXXXXXXXXXDEVILDYNSETIPQIS 266
LCI+VNNR+LFFVASESSYNEN IN+PKEIDDTR DEVILDYNS+ IP +S

Sbjct: 434 LCIKVNNRDLFFVASESSYNENGINSPEKEDDTITNNNNYKKNLDEVILDYNSDAIPNLS 493

Query: 267 NQTLNTLVQDDSYVPRYDSNGTSEIEHNVDLNFFYLHAQKVPEGETNISLTSSIDTA 326
++ LNT Q+DSYVP+YDSNGTSEI+E+ V LNVFFYL+AQK PEGE+ ISLTSS++TA

Sbjct: 494 SRLLNTTAQNDSYVPKYDSNGTSEIKEYTDKLNFFYLYAQKAPEGEASISLTSSVNTA 553

Query: 327 LSEESQVYTFSSSEFINTINKPVHAALFISWINQVIRDFTEATQKSTFDKIADISLVP 386
L + S+VYTFSS+FINT+NKPV AALFISWI QVI DFTTEATQKST DKIADISL+VP

Sbjct: 554 LLDASKVYTFSSDFINTVNKPVQAALFISWIQQVINDFTTEATQKSTIDKIDIADISLIVP 613

Query: 387 YVGLALNIGNEVQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFISFIGSSEXXXX 446
YVGLALNIGNEVQK NFKEA ELLGAGILLEFVPELLIPTILVFTIKSFI S +

Sbjct: 614 YVGLALNIGNEVQKGNFKEAIELLGAGILLEFVPELLIPTILVFTIKSFINSDDSKNII 673

Query: 447 XXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKYN 506
+L ERE KWKE+YSWIVSNWLTRINTQFNKRKEQMYQALQNQVD IK +IEYKYN

Sbjct: 674 KAINNALRERELKWKEVYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDGIKKIIIEYKYN 733

Query: 507 NYTSDERNRLESEYNINNNIREELKKVSLAMENIERFITESSIFYLMKLINEAKVSKLRE 566
NYT DE+NRL +EYNI +I+EELNKKVSLAM+NI+RF+TESSI YLMKLINEAK++KL E

Sbjct: 734 NYTLDEKNRLRAEYNIYSIKEELNKKVSLAMQNIDRFLTESSISYLMKLINEAKINKLSE 793

Query: 567 YDEGVKEYLLDYISEHRSILG-NSVQELNDLVTSTLNNSIPFELSSYTNDKILI 619

YD+ V +YLL+YI E+ S LG +SV ELN+LV++TLNNSIPFELS YTNDKILI

Sbjct: 794 YDKRVNQYLLNYILENSSTLGTSSVPELNNLVSNTLNNSIPFELSEYTNDKILI 847

>gi 9650999 dbj BAB03512.1	type E botulinum toxin [Clostridium butyricum]
gi 9651001 dbj BAB03513.1	type E botulinum toxin [Clostridium butyricum]
gi 9651003 dbj BAB03514.1	type E botulinum toxin [Clostridium butyricum]
gi 9651005 dbj BAB03515.1	type E botulinum toxin [Clostridium butyricum]
gi 9651007 dbj BAB03516.1	type E botulinum toxin [Clostridium butyricum]
gi 9651009 dbj BAB03517.1	type E botulinum toxin [Clostridium butyricum]
gi 9651011 dbj BAB03518.1	type E botulinum toxin [Clostridium butyricum]
gi 9651013 dbj BAB03519.1	type E botulinum toxin [Clostridium butyricum]

gi 9651015 dbj BAB03520.1	type E botulinum toxin [Clostridium butyricum]
gi 9651017 dbj BAB03521.1	type E botulinum toxin [Clostridium butyricum]
gi 9651019 dbj BAB03522.1	type E botulinum toxin [Clostridium butyricum]

Length = 1251

Score = 565 bits (1457), Expect = e-160
Identities = 289/416 (69%), Positives = 350/416 (84%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKIEDDTXXXXXXXXXDEVILDYNSETIPQIS 266
+CI +NN ELFFVASE+SYN++INTPKIEDDT D+VIL++NSE+ P +S
Sbjct: 425 ICIEINNGELFFVASENSYNNDDNINTPKIEDDTVTSNNNYENDLDQVILNFNSESAPGLS 484

Query: 267 NQLTNLTVQDDSYVPRYDSNGTSEIEEHNVVDLNFFYLHAQKVP EGETNISLTSSIDTA 326
++ LN +Q+D+Y+P+YDSNGTS+IE+H+V +LNVFFYL AQKVP EGE N++LTSSIDTA
Sbjct: 485 DEKLNLTIONDAYI PKYDSNGTSDIEQHDVNELNVFFYLDAQKVP EGENNVNLTSSIDTA 544

Query: 327 LSEESQVYTFSSSEFIN TINKPVHAALFISWINQVIRDFTTEATQKSTFDKIADISLVVP 386
L E+ ++YTFFSSEFIN +NKPV AALF+SWI QV+ DFTTEA QKST DKIADIS+VVPP
Sbjct: 545 LLEOPKIYTFSSSEFINNVNKPVOAALFVSWIOOVLVDFTTEANOKSTVDKIADISIVVP 604

Query: 387 YVGLALNIGNEVKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSSEXXXXXX 446
Y+GLALNIGNE QK NFK+A ELLGAGILLEFVPELLIPTILVFTIKSF+GSS+
Sbjct: 605 YIGLALNIGNEAQKGNEFKDAELLGAGILLEFVPELLIPTILVFTIKSFIGSSEDNKNV 664

Query: 447 XXXXSLMERETKWEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKYN 506
+L ER+ KWKE+YS+IVSNW+T+INTQFNKRKEQMYQALQNQV+A+KT+IE+KYN
Sbjct: 665 KAINNALKERDEKWKEVYSELIVSNWMTKINTOENKRKEQMYQALQNQVNAIKTILEEKYN 724

Query: 507 NYTSDERNRLSEYNNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLRE 566
+YT +E+ L++ Y+I I ELN+KVS+AM NI+RF+TESSI YLMKLINE K++KLRE
Subject: 725 SYTLEEKKEIKNNDLIEOLENEI NOKVSIAMNNIDRELTTESSISYLMKLINEVKINKLRE 784

Query: 567 YDEGVKEYLLDYI SEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
YDE VK YLLDYI +H SILG S QELN +V TLNNNSIPF+LSSYT+DKILI YF
Sbjct: 785 YDENNUKTYLIDYI LOUCSILGECOELNSMVIETLNNSIPFELSSYTNDKILILYF 840

gi|98569|pir|S21178 botulinum neurotoxin type E precursor - Clostridium botulinum
gi|40398|emb|CAA44558.1| botulinum neurotoxin type E [Clostridium botulinum]
gi|19744173|gbj|BAB86845.1| botulinum neurotoxin type E [Clostridium botulinum]
Length = 1252

Score = 564 bits (1453), Expect = e-159
Identities = 290/416 (69%), Positives = 350/416 (84%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKEIDDTXXXXXXXXXDEVILDYNSETIPQIS 266
 +CI +NN ELFFVASE+SYN++INTPKEIDDT D+VIL++NSE+ P +S
 Sbjct: 425 ICIEINNGELFFVASESENSYNDNINTPKEIDDTVTSNNNYENDLDOVILNFENSEAPGIL 484

Query: 267 NQLNLTQVQDDSYVPRYDSNGTSEIEHNVDLNVFFYLHAQKVPEGETNISLTSSIDTA 326
+ + LN +Q+D+Y+P+YDSNGTS+IE+H+V +LNVFFYL AQKVPEGE N++LTSSIDTA
Sbjct: 485 DEKINLTQVQDDSYVPRYDSNGTSEIEHNVDLNVFFYLHAQKVPEGETNISLTSSIDTA 544

Query: 327 LSEESQVYTFSSEFINTINKPVHAALFISWINQVIRDFTEATQKSTFDKIADISLVVP 386
L E+ ++YTFFSSEFIN+NKPV AALF+SWI QV+ DFTTEA QKST DKIADIS+VVP
Subject: 545 LLFORKLYTTEESSEFINNNKPVQANLIVSWLQOVLVDETTAEQKSTVDKIADISLVVP 604

Query: 387 YVGLALNIGNEVKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSXXXXXX 446
Y+GLALNIGNE QK NFK+A ELLGAGILLEF PELLIPITLVFTIKSF+GSS+
Subject: 605 YVGLALNIGNEVKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSXXXXXX 664

Query: 447 XXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKYN 506
+L ER+ KWKE+YS+IVSNW+T+INTQFNKRKEQMYQALQNQV+AIKT+IE KYN

CHAP. 5:67. NYTSDEBNIESEXYNNINIPEELNKVSLAMENIEBEITESSELEYLMKLINENAKVSKIRE. EGG

+YT +E+N L ++Y+I I ELN+KVS+AM NI+RF+TESSI YLMKLINE K++KLRE
 Sbjct: 725 SYTLEEKNELTNKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLRE 784

Query: 567 YDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
 YDE VK YLL+YI +H SILG S QELN +VT TLNNSIPF+LSSYT+DKILI YF
 Sbjct: 785 YDENVKTYLLNYIIQHGSILGESQQELNSMVTDTLNNSIPFKLSSYTDDKILISYF 840

>gi|399135|sp|Q00496|EXE_CLOBO Botulinum neurotoxin type E precursor (BoNT/E) (B
 gi|40394|emb|CAA43999.1| botulinum neurotoxin type E [Clostridium botulinum]
 Length = 1251

Score = 563 bits (1451), Expect = e-159
 Identities = 289/416 (69%), Positives = 350/416 (84%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKEIDDXTXXXXXXXXXDEVILDYNSETIPQIS 266
 +CI +NN ELFFVASE+SYN+++INTPKEIDDT D+VIL++NSE+ P +S
 Sbjct: 425 ICIEINNGELFFVASENSYNDDNINTPKEIDDVTSNNNYENDLDQVILNFNSEAPGLS 484

Query: 267 NQTLNTLVQDDSYVPRYDSNGTSEIEHNVDLNFFYLHAQKVPEGETNISLTSSIDTA 326
 ++ LN +Q+D+Y+P+YDSNGTS+IE+H+V +LNVFFYL AQKVPEGE N++LTSSIDTA
 Sbjct: 485 DEKLNLTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTA 544

Query: 327 LSEESQVYTFSSSEFIN TINKPVHAALFISWINQVIRDFTEATQKSTFDKIADISLVVP 386
 L E+ ++YTFFSSEFIN +NKPV AALF+SWI QV+ DFTTEA QKST DKIADIS+VVP
 Sbjct: 545 LLEQPKIYTFFSSEFINNVNKPVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVVP 604

Query: 387 YVGLALNIGNEVQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFFIGSSEXXXXXX 446
 Y+GLALNIGNE QK NFK+A ELLGAGILLEF PELLIPITLVFTIKSF+GSS+
 Sbjct: 605 YIGLALNIGNEAQKGNFKDALELLGAGILLEFEPELLIPTILVFTIKSFGLSSDNKNKVI 664

Query: 447 XXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKYN 506
 +L ER+ KWKE+YS+IVSNW+T+INTQFNKRKEQMYQALQNQV+AIKT+IE KYN
 Sbjct: 665 KAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQNQVNAIKTIIESKYN 724

Query: 507 NYTSDERNRLESEYNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLRE 566
 +YT +E+N L ++Y+I I ELN+KVS+AM NI+RF+TESSI YLMK+INE K++KLRE
 Sbjct: 725 SYTLEEKNELTNKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLRE 784

Query: 567 YDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
 YDE VK YLL+YI +H SILG S QELN +VT TLNNSIPF+LSSYT+DKILI YF
 Sbjct: 785 YDENVKTYLLNYIIQHGSILGESQQELNSMVTDTLNNSIPFKLSSYTDDKILISYF 840

>gi|399136|sp|P30995|EXE_CLOBU Botulinum neurotoxin type E precursor (BoNT/E) (B
 gi|7438649|pir|JH0256 botulinum neurotoxin type E precursor - Clostridium butyri
 gi|40380|emb|CAA43998.1| botulinum neurotoxin [Clostridium butyricum]
 Length = 1251

Score = 559 bits (1440), Expect = e-158
 Identities = 287/416 (68%), Positives = 347/416 (83%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKEIDDXTXXXXXXXXXDEVILDYNSETIPQIS 266
 +CI +NN ELFFVASE+SYN+++INTPKEIDDT D+VIL++NSE+ P +S
 Sbjct: 425 ICIEINNGELFFVASENSYNDDNINTPKEIDDVTSNNNYENDLDQVILNFNSEAPGLS 484

Query: 267 NQTLNTLVQDDSYVPRYDSNGTSEIEHNVDLNFFYLHAQKVPEGETNISLTSSIDTA 326
 ++ LN +Q+D+Y+P+YDSNGTS+IE+H+V +LNVFFYL AQKVPEGE N++LTSSIDTA
 Sbjct: 485 DEKLNLTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTA 544

Query: 327 LSEESQVYTFSSSEFIN TINKPVHAALFISWINQVIRDFTEATQKSTFDKIADISLVVP 386
 L E+ ++YTFFSSEFIN +NKPV AALF+WI QV+ DFTTEA QKST DKIADIS+VVP
 Sbjct: 545 LLEQPKIYTFFSSEFINNVNKPVQAALFVGWIQQVLVDFTTEANQKSTVDKIADISIVVP 604

Query: 387 YVGLALNIGNEVQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFFIGSSEXXXXXX 446
 Y+GLALNIGNE QK NFK+A ELLGAGILLEF PELLIPITLVFTIKSF+GSS+
 Sbjct: 605 YIGLALNIGNEAQKGNFKDALELLGAGILLEFEPELLIPTILVFTIKSFGLSSDNKNKVI 664

Query: 447 XXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNVDAIKTVIEYKYN 506
 +L ER+ KWKE+YS+IVSNW+T+INTQFNKRKEQMYQALQNV+A+K +IE KYN

Sbjct: 665 KAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQNVNALKAIESKYN 724

Query: 507 NYTSDERNRLESEYNINNIREEELKKVSLAMENIERFITESSIFYLMKLINEAKVSKLRE 566
 +YT +E+N L ++Y+I I ELN+KVS+AM NI+RF+TESSI YLMKLINE K++KLRE

Sbjct: 725 SYTLEEKNELTNKYDIEQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLRE 784

Query: 567 YDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
 YDE VK YLLDYI +H SILG S QELN +V TLNNSSIPF+LSSYT+DKILI YF

Sbjct: 785 YDENVKTYLLDYIIKHGSILGESQQELNSMVIDTLNNSSIPFKLSSYTDDKILISYF 840

>gi|9955895|dbj|BAB12249.1| type E botulinum toxin [Clostridium butyricum]
 Length = 1255

Score = 559 bits (1440), Expect = e-158

Identities = 287/416 (68%), Positives = 347/416 (83%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKIEDDTXXXXXXXXXDEVILDYNSETIPQIS 266
 +CI +NN ELFFVASE+SYN+++INTPKIEDDT D+VIL++NSE+ P +S

Sbjct: 428 ICIEINNGELFFVASENSYNDDNINTPKIEDDTVTSNNNYENDLDQVILNFNSEAPGLS 487

Query: 267 NQTLNTLVQDDSYVPRYDSNGTSEIEHHNVVDLNFFYLHAQKVPEGETNISLTSSIDTA 326
 ++ LN +Q+D+Y+P+YDSNGTS+IE+H+V +LNVFFYL AQKVPEGE N++LTSSIDTA

Sbjct: 488 DEKLNLTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTA 547

Query: 327 LSEESQVYTFSSSEFIN TINKPVHAALFISWINQVIRDFTEATQKSTFDKIADISLVVP 386
 L E+ ++YTFFSSEFIN +NKPV AALF+ WI QV+ DFTTEA QKST DKIADIS+VVP

Sbjct: 548 LLEQPKIYTFFSSEFINNVNKPVQAALFVGWIQQVLVDFTTEANQKSTVDKIADISIVVP 607

Query: 387 YVGLALNIGNEVQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFFIGSSEXXXXX 446
 Y+GLALNIGNE QK NFK+A ELLGAGILLEF PELLIPITLVFTIKSF+GSS+

Sbjct: 608 YIGLALNIGNEAQKGNFKDALELLGAGILLEFEPELLIPTILVFTIKSFGLGSSDNKNKVI 667

Query: 447 XXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNVDAIKTVIEYKYN 506
 +L ER+ KWKE+YS+IVSNW+T+INTQFNKRKEQMYQALQNV+A+K +IE KYN

Sbjct: 668 KAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQNVNALKAIESKYN 727

Query: 507 NYTSDERNRLESEYNINNIREEELKKVSLAMENIERFITESSIFYLMKLINEAKVSKLRE 566
 +YT +E+N L ++Y+I I ELN+KVS+AM NI+RF+TESSI YLMKLINE K++KLRE

Sbjct: 728 SYTLEEKNELTNKYDIEQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLRE 787

Query: 567 YDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
 YDE VK YLLDYI +H SILG S QELN +V TLNNSSIPF+LSSYT+DKILI YF

Sbjct: 788 YDENVKTYLLDYIIKHGSILGESQQELNSMVIDTLNNSSIPFKLSSYTDDKILISYF 843

>gi|21832314|dbj|BAC05434.1| type E botulinum toxin [Clostridium butyricum]
 Length = 1252

Score = 559 bits (1440), Expect = e-158

Identities = 287/416 (68%), Positives = 347/416 (83%)

Query: 207 LCIRVNNRELFFVASESSYNENDINTPKIEDDTXXXXXXXXXDEVILDYNSETIPQIS 266
 +CI +NN ELFFVASE+SYN+++INTPKIEDDT D+VIL++NSE+ P +S

Sbjct: 425 ICIEINNGELFFVASENSYNDDNINTPKIEDDTVTSNNNYENDLDQVILNFNSEAPGLS 484

Query: 267 NQTLNTLVQDDSYVPRYDSNGTSEIEHHNVVDLNFFYLHAQKVPEGETNISLTSSIDTA 326
 ++ LN +Q+D+Y+P+YDSNGTS+IE+H+V +LNVFFYL AQKVPEGE N++LTSSIDTA

Sbjct: 485 DEKLNLTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTA 544

Query: 327 LSEESQVYTFSSSEFIN TINKPVHAALFISWINQVIRDFTEATQKSTFDKIADISLVVP 386
 L E+ ++YTFFSSEFIN +NKPV AALF+ WI QV+ DFTTEA QKST DKIADIS+VVP

Sbjct: 545 LLEQPKIYTFFSSEFINNVNKPVQAALFVGWIQQVLVDFTTEANQKSTVDKIADISIVVP 604

Query: 387 YVGLALNIGNEVKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSSEXXXXXX 446
 Y+GLALNIGNE QK NFK+A ELLGAGILLEF PELLIPPTILVFTIKSF+GSS+
 Sbjct: 605 YIGLALNIGNEAQKGNFKDALELLGAGILLEFEPELLIPTILVFTIKSFLGSSDNKNKVI 664

Query: 447 XXXXXSLMERETKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKYN 506
 +L ER+ KWKE+YS+IVSNW+T+INTQFNKRKEQMYQALQNQV+A+K +IE KYN
 Sbjct: 665 KAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQNQVNALKAIIESKYN 724

Query: 507 NYTSDERNRLESEYNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLRE 566
 +YT +E+N L ++Y+I I ELN+KVS+AM NI+RF+TESSI YLMKLINE K++KLRE
 Sbjct: 725 SYTLEEKNELTNKYDIEQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLRE 784

Query: 567 YDEGVKEYLLDYISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
 YDE VK YLLDYI +H SILG S QELN +V TLNNSSIPF+LSSYT+DKILI YF
 Sbjct: 785 YDENVKTYLLDYIikhgsilgesqqelnsmvidtlnnsipfkllssytddkilisyf 840

>gi|1084233|pir||S48110 neurotoxin type F - Clostridium botulinum (fragment)
gi|407793|emb|CAA50152.1 botulinum neurotoxin type F [Clostridium botulinum]
 Length = 366

Score = 392 bits (1006), Expect = e-107
 Identities = 214/225 (95%), Positives = 214/225 (95%)

Query: 398 VQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSSEXXXXXXXXXSLMERE 457
 VQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSSE SLMERE
 Sbjct: 1 VQKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSENKNKIIKAINNSLMERE 60

Query: 458 TKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKNNYTSDERNRLE 517
 TKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKNNYTSDERNRLE
 Sbjct: 61 TKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKNNYTSDERNRLE 120

Query: 518 SEYNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLREYDEGVKEYLLD 577
 SEYNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLREYDEGVKEYLLD
 Sbjct: 121 SEYNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLREYDEGVKEYLLD 180

Query: 578 YISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 622
 YISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF
 Sbjct: 181 YISEHRSILGNSVQELNDLVTSTLNNSIPFELSSYTNDKILILYF 225

>gi|134649|sp|P28760|SQDM_BACCA Superoxide dismutase [Mn]
gi|98098|pir|S22053 superoxide dismutase (EC 1.15.1.1) (Mn) - Bacillus caldotenae
gi|39453|emb|CAA44556.1| Manganese superoxide dismutase [Bacillus caldotenax]
gi|7578509|gb|AAF64074.1|AF147780_1 superoxide dismutase [Geobacillus thermoleovo]
gi|384175|prf|1905285A superoxide dismutase
 Length = 204

Score = 387 bits (994), Expect = e-106
 Identities = 188/204 (92%), Positives = 188/204 (92%), Gaps = 16/204 (7%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDQLN----- 51
 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDQLN
 Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDQLQNSLELLSN 60

Query: 52 -----IRTAVRNNGGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 104
 IRTAVRNNGGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS
 Sbjct: 61 LEALPESIRTAVRNNGGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120

Query: 105 KAAAGRFGSGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 164
 KAAAGRFGSGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE
 Sbjct: 121 KAAAGRFGSGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180

Query: 165 YIAAFWNIWNDEVAKRYSEAKAK 188
 YIAAFWNIWNDEVAKRYSEAKAK
 Sbjct: 181 YIAAFWNIWNDEVAKRYSEAKAK 204

>gi|134650|sp|P00449|SODM_BACST Superoxide dismutase [Mn]
 gi|1070456|pir|DSBSNF superoxide dismutase (EC 1.15.1.1) (Mn) - Bacillus stearothermophilus
 gi|143203|gb|AAA22600.1 manganese superoxide dismutase (EC 1.15.1.1)
 gi|143552|gb|AAA22765.1 Mn-superoxide dismutase
 gi|143555|gb|AAA22767.1 Mn-superoxide dismutase
 Length = 204

Score = 386 bits (991), Expect = e-106
 Identities = 186/204 (91%), Positives = 188/204 (92%), Gaps = 16/204 (7%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQN----- 51
 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQN
 Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQNKSLLELLSN 60
 Query: 52 -----IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 104
 IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELA+AINKKFGSFTAFKDEFS
 Sbjct: 61 LEALPESIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELADAINKKFGSFTAFKDEFS 120
 Query: 105 KAAAGRGSGGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 164
 KAAAGRGSGGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE
 Sbjct: 121 KAAAGRGSGGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
 Query: 165 YIAAFWNIVNWDEVAKRYSEAKAK 188
 YIAAFWN+VNWDEVAKRYSEAKAK
 Sbjct: 181 YIAAFWNVNVNDEVAKRYSEAKAK 204

>gi|7798571|dbj|BAA95631.1 superoxide dismutase [Geobacillus thermoleovorans]
 Length = 204

Score = 382 bits (981), Expect = e-105
 Identities = 186/204 (91%), Positives = 186/204 (91%), Gaps = 16/204 (7%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQN----- 51
 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQN
 Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQNKSLLELLSN 60
 Query: 52 -----IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 104
 IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS
 Sbjct: 61 LEALPESIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 120
 Query: 105 KAAAGRGSGGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 164
 KAAAGRF_GWAWLNVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE
 Sbjct: 121 KAAAGRFSPGWAHLVNNGELEITSTPNQDSPIMEGKTPILGLDVWEHAYYLKYQNRRPE 180
 Query: 165 YIAAFWNIVNWDEVAKRYSEAKAK 188
 YIAAFWNIVNWDEVAKRYSEAKAK
 Sbjct: 181 YIAAFWNIVNWDEVAKRYSEAKAK 204

>gi|448837|prf||1918164A superoxide dismutase
 Length = 205

Score = 381 bits (979), Expect = e-104
 Identities = 186/205 (90%), Positives = 188/205 (91%), Gaps = 17/205 (8%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQN----- 51
 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQN
 Sbjct: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGHPDLQNKSLLELLSN 60
 Query: 52 -----IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELAEAINKKFGSFTAFKDEFS 104
 IRTAVRNNNGGHANHSLFWTILSPNGGEPTGELA+AINKKFGSFTAFKDEFS
 Sbjct: 61 LEALPESIRTAVRNNNGGHANHSLFWTILSPNGGEPTGELADAINKKFGSFTAFKDEFS 120
 Query: 105 KAAAGRGSGGWAHLVNNGELEITSTPNQDS-PIMEGKTPILGLDVWEHAYYLKYQNRRP 163
 KAAAGRGSGGWAHLVNNGELEITSTPNQDS PIMEGKTPILGLDVWEHAYYLKYQNRRP

Sbjct: 121 KAAAGRGSGWAWLVVNNGELEITSTPNQDSPPIMEGKTPILGLDVWEHAYYLKYQNRRP 180

Query: 164 EYIAAFWNIVNWDEVAKRYSEAKAK 188

EYIAAFWN+VNWDEVAKRYSEAKAK

Sbjct: 181 EYIAAFWNVNVNWDEVAKRYSEAKAK 205

<input type="checkbox"/>	>gi 7438650 pir S48109	neurotoxin type F - Clostridium botulinum (fragment)
gi	407789 emb CAA50147.1	botulinum neurotoxin type F [Clostridium botulinum]
gi	407791 emb CAA50151.1	botulinum neurotoxin type F [Clostridium botulinum]

Length = 369

Score = 330 bits (847), Expect = 3e-89

Identities = 179/224 (79%), Positives = 193/224 (86%)

Query: 399 QKENFKEAFELLGAGILLEFVPELLIPTILVFTIKSFIGSSEXXXXXXXXXXSLMERET 458
+K NF+EAFELLG GILLEFVPEL IP ILVFTIKS+I S E SL+ERE

Sbjct: 2 EKGNFEEAFELLGVGILLEFVPELTIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREA 61

Query: 459 KWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTVIEYKYNNTSDERNLES 518

KWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKT IEYKYNNTSDER+NRLES

Sbjct: 62 KWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTAIEYKYNNTSDERKNRLES 121

Query: 519 EYNINNIREELNKKVSLAMENIERFITESSIFYLMKLINEAKVSKLREYDEGVKEYLLDY 578
EYNINNI EELNKKVSLAM+NIERF+TESSI YLMKLINEAKV KL++YD VK LL+Y

Sbjct: 122 EYNINNIEELNKKVSLAMKNIERFMTESSISYLMKLINEAKVGKLKKYDNHVKS DLLNY 181

Query: 579 ISEHRSILGNSVQELNDLVSTLNNSIPFELSSYTNDKILILYF 622

I +HRSILG EL+DLVTSTLN+SIPFELSSYTNDKILI+YF

Sbjct: 182 ILDHRSILGEQTNELSDLVTSTLNSSIPFELSSYTNDKILIYF 225

<input type="checkbox"/>	>gi 15613972 ref NP_242275.1	superoxide dismutase [Bacillus halodurans]
gi	25285807 pir A83826	superoxide dismutase sodA [imported] - Bacillus halodurans C-125)
gi	10174025 dbj BAB05128.1	superoxide dismutase [Bacillus halodurans]

Length = 202

Score = 327 bits (838), Expect = 4e-88

Identities = 153/202 (75%), Positives = 170/202 (84%), Gaps = 16/202 (7%)

Query: 1 MPFELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDL----- 49
M FELP LPYP +ALEPHID+ TMNIHH KHHNTYVT LNAALEGH L

Sbjct: 1 MAFELPKLPYPANALEPHIDEATMNIHHGKHHNTYVTKLNAALEGH SIEALVSD 60

Query: 50 -----QNIRTAVRNNGGGHANHSFWTILSPNGGEPTGELAEAINKKFGSFTA FKDEFS 104

+NIRTAVRNNGGGHAN+LFW ILSPNGGG PTGELA+AIN +FGSF FK++F+

Sbjct: 61 LDAVPENIRTAVRNNGGGHANHTLFWQILSPNGGGAPTGELADAINAEFGSF DQFKEKFA 120

Query: 105 KAAAGRGSGWAWLVVNNGELEITSTPNQDSPPIMEGKTPILGLDVWEHAYYLKYQNRRPE 164

AAA RFGSGWAWL VN+G+LEITSTPNQD+P+MEGKTPILGLDVWEHAYYL YQNRRP+

Sbjct: 121 DAAANRGSGWAWL VVNDGKLEITSTPNQDTPLMEGKTPILGLDVWEHAYYL NYQNRRPD 180

Query: 165 YIAAFWNIVNWDEVAKRYSEAK 186

YI+AFWN+VNWDEVAKRY+EAK

Sbjct: 181 YISAFWNVNVNWDEVAKRYNEAK 202

<input type="checkbox"/>	>gi 30264347 ref NP_846724.1	superoxide dismutase, Mn [Bacillus anthracis str.
gi	30259005 gb AAP28210.1	superoxide dismutase, Mn [Bacillus anthracis str. Ames

Length = 203

Score = 318 bits (815), Expect = 2e-85

Identities = 148/199 (74%), Positives = 163/199 (81%), Gaps = 16/199 (8%)

Query: 4 ELPALPYPYDALEPHIDKETMNIHHTKHHNTYVTNLNAALEGH PDLQN----- 51

ELP LPY YDALEPH DKETMNIHHTKHHNTY+TNLNAALEGH +L +

Sbjct: 5 ELPNLPYAYDALEPHFDKETMNIHHTKHHNTYITNLNAALEGH AELADKSVEELVANLNE 64

Animal Cell Lines

ATCC No.	Species	Name	Tissue Source	Cell Type	Appearance
CRL-11179	mouse	CATH.a	brain	neuron	neuronal and amoeboid
CCL-131	mouse	Neuro-2a	brain; neuroblastoma	neuroblast	neuroblast
CCL-147	mouse	NB41A3	brain; neuroblastoma	neuroblast	neuroblast
CRL-2263	mouse	N1E-115	brain; neuroblastoma	neuroblast	neuroblast
HB-12317	mouse (neuroblastoma); rat (glioma)	NG108-15	brain; glioblastoma; neuroblastoma; hybrid	glial cell; neuron	flat; round
CRL-2534	mouse	C8-D30	brain; cerebellum	astrocyte, type III phenotype	neuronal
CRL-2535	mouse	C8-S	brain; cerebellum	astrocyte, type II phenotype	neuronal
CRL-2540	mouse	C8-B4	brain; cerebellum	microglial	neuronal
CRL-2541	mouse	C8-D1A	brain; cerebellum	astrocyte, type I phenotype	neuronal
CRL-1443	mouse	BC3H1	brain; smooth muscle like; tumor	endothelial	endothelial
CRL-2299	mouse	bEnd.3	brain; cerebral cortex; endothelioma	microglia; macrophage	macrophage
CRL-2467	mouse	EOC 2	brain	microglia; macrophage	macrophage
CRL-2468	mouse	EOC 13.31	brain	microglia; macrophage	macrophage
CRL-2469	mouse	EOC 20	brain	glial cell	fibroblast
CCL-107	rat	C6	brain; glioma	glial cell	fibroblast
CRL-2199	rat	C6/LacZ	brain; glioma	glial cell	fibroblast
CRL-2303	rat	C6/lacZ7	brain; glioma	glial cell	fibroblast
CRL-2397	rat	F98	brain; undifferentiated malignant glioma	glial	glial
CRL-2433	rat	RG2 (D74)	brain; undifferentiated malignant glioma	glial	glial
CRL-2200	rat	9L/lacZ	brain; gliosarcoma	astrocyte, type I phenotype	fibroblast
CRL-2005	rat	DI-TNC1	brain; diencephalon; normal	astrocyte, type I phenotype	fibroblast
CRL-2006	rat	CTX-TNA2	brain; cortex; normal	astrocyte, type I phenotype	fibroblast
CRL-1721	rat	PC-12	pheochromocytoma; adrenal gland	polygonal	glial, astrocyte
CRL-2032	cat	PG-4 (S+L)	brain; normal	astrocyte	glial, astrocyte
CRL-2033	cat	G355-5	brain; normal	astrocyte	
CRL-1656	ferret	Mpf	brain; normal		
CRL-1700	ovine	SCP	brain; choroid plexus		
CRL-6538	ovine	OA1	brain; normal		
CRL-2532	Japanese quail	QNR/D	neuroretina		
CRL-2533	Japanese quail	QNR/K2	neuroretina	neuronal astroglial	fibroblast

For more information or to place an order:

Phone: 800-638-6597

703-365-2700

Fax: 703-365-2750

E-mail: sales@atcc.org

Use our online shopping cart at:

www.atcc.org

These products are intended for laboratory research purposes only. They are not intended for use in humans.

© Copyright 2001. American Type Culture Collection. All rights reserved. ATCC® is a registered trademark of American Type Culture Collection.



Neurobiology Cell Line Collection

ATCC No.	Species	Name	Tissue Source	Cell Type	Appearance
Non-tumor, neuronal-like cells					
CRL-10442	human	HCN-1A	brain	cortical neuron	neuronal
CRL-10742	human	HCN-2	brain	cortical neuron	neuronal
Tumor-derived neuronal-like cells					
CCL-127	human	IMR-32	brain; neuroblastoma	neuroblast	fibroblast;neuroblast
CRL-1718	human	CCF-STTG1	brain; astrocytoma	fibroblast	astrocytic
CRL-2060	human	PFSK-1	brain; cerebellum; malignant primitive neuroectodermal tumor	neuroblast	
CRL-2137	human	SK-N-AS	brain; neuroblastoma	neuroblast	epithelial
CRL-2142	human	SK-N-FI	brain; neuroblastoma	neuroblast	epithelial
CRL-2149	human	SK-N-DZ	brain; neuroblastoma	neuroblast	epithelial
CRL-2266	human	SH-SY5Y	brain; neuroblastoma	neuroblast	epithelial
CRL-2267	human	BE(2)-M17	brain; neuroblastoma	neuroblast	neuroblast
CRL-2268	human	BE(2)-C	brain; neuroblastoma	neuroblast	neuroblast
CRL-2270	human	MC-IXC	brain; neuroblastoma	neuroblast	fibroblast
CRL-2271	human	SK-N-BE(2)	brain; neuroblastoma	neuroblast	neuroblast
CRL-2273	human	CHP-212	brain; neuroblastoma	astroglia	neuroblast
CRL-8621	human	SVG p12	brain	astroglia	fibroblast
HTB-10	human	SK-N-MC	brain; neuroepithelioma, metastatic site: supra-orbital area	astroglia	epithelial
HTB-11	human	SK-N-SH	brain; neuroblastoma, metastatic site: bone marrow	astroglia	epithelial
HTB-12	human	SW-1088	brain; astrocytoma	astroglia	epithelial
HTB-13	human	SW-1783	brain; astrocytoma	astroglia	fibroblast
HTB-15	human	U-118 MG	brain; glioblastoma; astrocytoma	astroglia	mixed
Glioblastoma and glioma cells					
CRL-1620	human	A172	brain; glioblastoma	glial cell	fibroblast
CRL-1690	human	T98G	brain; glioblastoma multiforme	glial cell	fibroblast
CRL-2020	human	DBTRG-05MG	brain; glioblastoma	glial cell	fibroblast
CRL-2365	human	M059K	brain; malignant glioblastoma; glioma	glial cell	fibroblast
CRL-2366	human	M059J	brain; malignant glioblastoma; glioma	glial cell	epithelial
CRL-7773	human	TE 615.T	brain; ganglioneuroblastoma	glial cell	fibroblast
HTB-138	human	Hs 683	brain; glioma	glial cell	epithelial
HTB-14	human	U-87 MG	brain; glioblastoma; astrocytoma	glial cell	fibroblast
HTB-148	human	H4	brain; neuroglioma	glial cell	epithelial
HTB-16	human	U-138 MG	brain; glioblastoma	glial cell	polygonal
Medulloblastoma-derived cells					
CRL-8805	human	TE671 subline No. 2	brain; cerebellum; medulloblastoma		epithelial
HTB-185	human	D283 Med	brain; cerebellum; medulloblastoma, metastatic site: peritoneum		epithelial
HTB-186	human	Daoy	brain; cerebellum; desmoplastic cerebellar medulloblastoma		polygonal
HTB-187	human	D341 Med	brain; cerebellum; medulloblastoma		spheroid
Retinoblastoma-derived cells					
HTB-169	human	WERI-Rb-1	retinoblastoma; eye; retina		grape-like clusters of round cells
HTB-18	human	Y79	retinoblastoma; eye; retina		multipolar clusters
Neuroendocrine tissue					
CRL-5813	human	NCI-H660	lung; carcinoma; small cell lung cancer extrapulmonary origin (prostate), metastatic site: lymph node	neuroendocrine	epithelial
CRL-5893	human	NCI-H1770	lung; carcinoma; non-small cell lung cancer; metastatic site: lymph node	neuroendocrine	floating aggregates of round cells
CRL-2139	human	SK-PN-DW	malignant primitive neuroectodermal tumor; retroperitoneal embryonal tumor	neuroendocrine	epithelial
CRL-1973	human	NTERA-2:cl.D1	malignant pluripotent embryonal carcinoma; testis, metastatic site: lung		fibroblast